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<110> Baker, Kevin P.
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
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Paoni, Nicholas F.

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Arg Leu Arg Thr Val Leu Leu Asp Val Thr Asp Pro Glu Asn Val
80 85 90

Lys Arg Thr Ala Gln Trp Val Lys Asn Gln Val Gly Glu Lys Gly
95 100 105

Leu Trp Gly Leu Ile Asn Asn Ala Gly Val Pro Gly Val Leu Ala
110 115 120

Pro Thr Asp Trp Leu Thr Leu Glu Asp Tyr Arg Glu Pro Ile Glu
125 130 135

Val Asn Leu Phe Gly Leu Ile Ser Val Thr Leu Asn Met Leu Pro
140 145 150

Leu Val Lys Lys Ala Gln Gly Arg Val Ile Asn Val Ser Ser Val
155 160 165

Gly Gly Arg Leu Ala Ile Val Gly Gly Tyr Thr Pro Ser Lys
170 175 180

Tyr Ala Val Glu Gly Phe Asn Asp Ser Leu Arg Arg Asp Met Lys
185 190 195

Ala Phe Gly Val His Val Ser Cys Ile Glu Pro Gly Leu Phe Lys
 200 205 210
 Thr Asn Leu Ala Asp Pro Val Lys Val Ile Glu Lys Lys Leu Ala
 215 220 225
 Ile Trp Glu Gln Leu Ser Pro Asp Ile Lys Gln Gln Tyr Gly Glu
 230 235 240
 Gly Tyr Ile Glu Lys Ser Leu Asp Lys Leu Lys Gly Asn Lys Ser
 245 250 255
 Tyr Val Asn Met Asp Leu Ser Pro Val Val Glu Cys Met Asp His
 260 265 270
 Ala Leu Thr Ser Leu Phe Pro Lys Thr His Tyr Ala Ala Gly Lys
 275 280 285
 Asp Ala Lys Ile Phe Trp Ile Pro Leu Ser His Met Pro Ala Ala
 290 295 300
 Leu Gln Asp Phe Leu Leu Lys Gln Lys Ala Glu Leu Ala Asn
 305 310 315
 Pro Lys Ala Val

<210> 11
 <211> 2720
 <212> DNA
 <213> Homo sapines

<400> 11
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 gccccttggg ccgtcgccac cactgttagtc atgtacccac cgccgcccgc 150
 gccgcctcat cgggacttca tctcggtgac gctgagctt ggcgagagct 200
 atgacaacag caagagttgg cggcggcgct cgtgctggag gaaatggaag 250
 caactgtcga gattgcagcg gaatatgatt ctcttcctcc ttgcctttct 300
 gctttctgt ggactcctct tctacatcaa cttggctgac cattggaaag 350
 ctctggcttt caggctagag gaagagcaga agatgaggcc agaaaattgct 400
 gggtaaaac cagcaaatcc acccgcttta ccagtcctc agaaggcgga 450
 caccgaccct gagaacttac ctgagatttc gtcacagaag acacaaagac 500
 acatccagcg gggaccacct cacctgcaga ttagacccccc aagccaagac 550
 ctgaaggatg ggaccaggaa ggaggccaca aaaaggcaag aagccctgt 600
 ggatccccgc ccggaaggag atccgcagag gacagtcatc agctggaggg 650

gagcggtgat cgagcctgag cagggcacccg agtccccttc aagaagagca 700
gaagtgccca ccaagcctcc cctgccacccg gccaggacac agggcacacc 750
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<210> 12

<211> 699

<212> PRT

<213> Homo sapiens

<220>

<221> TRANSMEM

<222> 21-40 and 84-105

<223> Transmembrane Domain (type II)

<400> 12

Met	Ala	Ala	Cys	Glu	Gly	Arg	Arg	Ser	Gly	Ala	Leu	Gly	Ser	Ser
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Gln	Ser	Asp	Phe	Leu	Thr	Pro	Pro	Val	Gly	Gly	Ala	Pro	Trp	Ala
				20					25				30	

Val	Ala	Thr	Thr	Val	Val	Met	Tyr	Pro						
				35				40				45		

His	Arg	Asp	Phe	Ile	Ser	Val	Thr	Leu	Ser	Phe	Gly	Glu	Ser	Tyr
				50					55			60		

Asp	Asn	Ser	Lys	Ser	Trp	Arg	Arg	Ser	Cys	Trp	Arg	Lys	Trp	
				65				70			75			

Lys	Gln	Leu	Ser	Arg	Leu	Gln	Arg	Asn	Met	Ile	Leu	Phe	Leu	Leu
				80				85				90		

Ala	Phe	Leu	Leu	Phe	Cys	Gly	Leu	Leu	Phe	Tyr	Ile	Asn	Leu	Ala
				95					100			105		

Asp His Trp Lys Ala Leu Ala Phe Arg Leu Glu Glu Glu Gln Lys
 110 115 120
 Met Arg Pro Glu Ile Ala Gly Leu Lys Pro Ala Asn Pro Pro Val
 125 130 135
 Leu Pro Ala Pro Gln Lys Ala Asp Thr Asp Pro Glu Asn Leu Pro
 140 145 150
 Glu Ile Ser Ser Gln Lys Thr Gln Arg His Ile Gln Arg Gly Pro
 155 160 165
 Pro His Leu Gln Ile Arg Pro Pro Ser Gln Asp Leu Lys Asp Gly
 170 175 180
 Thr Gln Glu Glu Ala Thr Lys Arg Gln Glu Ala Pro Val Asp Pro
 185 190 195
 Arg Pro Glu Gly Asp Pro Gln Arg Thr Val Ile Ser Trp Arg Gly
 200 205 210
 Ala Val Ile Glu Pro Glu Gln Gly Thr Glu Leu Pro Ser Arg Arg
 215 220 225
 Ala Glu Val Pro Thr Lys Pro Pro Leu Pro Pro Ala Arg Thr Gln
 230 235 240
 Gly Thr Pro Val His Leu Asn Tyr Arg Gln Lys Gly Val Ile Asp
 245 250 255
 Val Phe Leu His Ala Trp Lys Gly Tyr Arg Lys Phe Ala Trp Gly
 260 265 270
 His Asp Glu Leu Lys Pro Val Ser Arg Ser Phe Ser Glu Trp Phe
 275 280 285
 Gly Leu Gly Leu Thr Leu Ile Asp Ala Leu Asp Thr Met Trp Ile
 290 295 300
 Leu Gly Leu Arg Lys Glu Phe Glu Glu Ala Arg Lys Trp Val Ser
 305 310 315
 Lys Lys Leu His Phe Glu Lys Asp Val Asp Val Asn Leu Phe Glu
 320 325 330
 Ser Thr Ile Arg Ile Leu Gly Gly Leu Leu Ser Ala Tyr His Leu
 335 340 345
 Ser Gly Asp Ser Leu Phe Leu Arg Lys Ala Glu Asp Phe Gly Asn
 350 355 360
 Arg Leu Met Pro Ala Phe Arg Thr Pro Ser Lys Ile Pro Tyr Ser
 365 370 375
 Asp Val Asn Ile Gly Thr Gly Val Ala His Pro Pro Arg Trp Thr
 380 385 390
 Ser Asp Ser Thr Val Ala Glu Val Thr Ser Ile Gln Leu Glu Phe

395	400	405
Arg Glu Leu Ser Arg Leu Thr Gly Asp Lys Lys Phe Gln Glu Ala		
410	415	420
Val Glu Lys Val Thr Gln His Ile His Gly Leu Ser Gly Lys Lys		
425	430	435
Asp Gly Leu Val Pro Met Phe Ile Asn Thr His Ser Gly Leu Phe		
440	445	450
Thr His Leu Gly Val Phe Thr Leu Gly Ala Arg Ala Asp Ser Tyr		
455	460	465
Tyr Glu Tyr Leu Leu Lys Gln Trp Ile Gln Gly Gly Lys Gln Glu		
470	475	480
Thr Gln Leu Leu Glu Asp Tyr Val Glu Ala Ile Glu Gly Val Arg		
485	490	495
Thr His Leu Leu Arg His Ser Glu Pro Ser Lys Leu Thr Phe Val		
500	505	510
Gly Glu Leu Ala His Gly Arg Phe Ser Ala Lys Met Asp His Leu		
515	520	525
Val Cys Phe Leu Pro Gly Thr Leu Ala Leu Gly Val Tyr His Gly		
530	535	540
Leu Pro Ala Ser His Met Glu Leu Ala Gln Glu Leu Met Glu Thr		
545	550	555
Cys Tyr Gln Met Asn Arg Gln Met Glu Thr Gly Leu Ser Pro Glu		
560	565	570
Ile Val His Phe Asn Leu Tyr Pro Gln Pro Gly Arg Arg Asp Val		
575	580	585
Glu Val Lys Pro Ala Asp Arg His Asn Leu Leu Arg Pro Glu Thr		
590	595	600
Val Glu Ser Leu Phe Tyr Leu Tyr Arg Val Thr Gly Asp Arg Lys		
605	610	615
Tyr Gln Asp Trp Gly Trp Glu Ile Leu Gln Ser Phe Ser Arg Phe		
620	625	630
Thr Arg Val Pro Ser Gly Gly Tyr Ser Ser Ile Asn Asn Val Gln		
635	640	645
Asp Pro Gln Lys Pro Glu Pro Arg Asp Lys Met Glu Ser Phe Phe		
650	655	660
Leu Gly Glu Thr Leu Lys Tyr Leu Phe Leu Leu Phe Ser Asp Asp		
665	670	675
Pro Asn Leu Leu Ser Leu Asp Ala Tyr Val Phe Asn Thr Glu Ala		
680	685	690

His Pro Leu Pro Ile Trp Thr Pro Ala
695

<210> 13
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 13
cgccagaagg gcgtgattga cgtc 24

<210> 14
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 14
ccatccttct tccagacag gccg 24

<210> 15
<211> 44
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-44
<223> Synthetic construct.

<400> 15
gaaggctgtg tccaggtct tcagtgagtg gtttggcctc ggtc 44

<210> 16
<211> 1524
<212> DNA
<213> Homo sapiens

<400> 16
ggcgccgcgt aggccccgga ggccggggccg gccgggctgc gagcgcctgc 50
cccatgcgcc gccgcctctc cgcacgatgt tcccctcgcg gagaaaagcg 100
gcgcagctgc cctgggagga cggcagggtcc gggttgctct ccggcggcct 150
ccctcgaaag tgttccgtct tccacctgtt cgtggcctgc ctctcgctgg 200
gcttcttctc cctactctgg ctgcagctca gctgctctgg ggacgtggcc 250

cgggcagtca gggacaagg gcaggagacc tcggccctc cccgtgcctg 300
ccccccagag ccgcggccctg agcactggga agaagacgca tcctggggcc 350
cccaccgcct ggcagtgctg gtgccttcc gcgaacgctt cgaggagctc 400
ctggtcttcg tgccccacat gcgcgccttc ctgagcagga agaagatccg 450
gcaccacatc tacgtgctca accaggtgga ccacttcagg ttcaaccggg 500
cagcgctcat caacgtggc ttcctggaga gcagcaacag cacggactac 550
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ctctctacca ctacaagacc tatgtcggcg gcattctgct gctctccaag 700
cagcaactacc ggctgtgcaa tggatgtcc aaccgcttct gggctgggg 750
ccgcgaggac gacgagttct accggcgcat taaggagct gggctccagc 800
ttttccgccc ctggaaatc acaactgggt acaagacatt tcgcccacctg 850
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cgggaccccc cctgccttcc tgctcaccct actctgaccc cttcacgt 1350
cccaggcctg tggtagtgg ggagggctga acaggacaac ctctcatcac 1400
cctactctga ctccttcac gtgcggcaggc ctgtggtag tggggagggc 1450
tgaacagagac aacctctcat caccccaaaa aaaaaaaaaa aaaaaaaaaa 1500
aaaaaaaaaa aaaaaaaaaa aaaa 1524

<210> 17
<211> 327
<212> PRT
<213> Homo sapiens

<220>

<221> sig_peptide
 <222> 1-42
 <223> Signal peptide.

<220>
 <221> misc_feature
 <222> 19-25,65-71,247-253,285-291,303-310
 <223> N-myristoylation site.

<220>
 <221> misc_feature
 <222> 27-31
 <223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

<220>
 <221> TRANSMEM
 <222> 29-49
 <223> Transmembrane domain (type II).

<220>
 <221> misc_feature
 <222> 154-158
 <223> N-glycosylation site.

<220>
 <221> misc_feature
 <222> 226-233
 <223> Tyrosine kinase phosphorylation site.

<400> 17

Met	Phe	Pro	Ser	Arg	Arg	Lys	Ala	Ala	Gln	Leu	Pro	Trp	Glu	Asp
1														15

Gly	Arg	Ser	Gly	Leu	Leu	Ser	Gly	Gly	Leu	Pro	Arg	Lys	Cys	Ser
														30
20														

Val	Phe	His	Leu	Phe	Val	Ala	Cys	Leu	Ser	Leu	Gly	Phe	Phe	Ser
														45
35														

Leu	Leu	Trp	Leu	Gln	Leu	Ser	Cys	Ser	Gly	Asp	Val	Ala	Arg	Ala
														60
50														

Val	Arg	Gly	Gln	Gly	Gln	Glu	Thr	Ser	Gly	Pro	Pro	Arg	Ala	Cys
														75
65														

Pro	Pro	Glu	Pro	Pro	Pro	Glu	His	Trp	Glu	Glu	Asp	Ala	Ser	Trp
														90
80														

Gly	Pro	His	Arg	Leu	Ala	Val	Leu	Val	Pro	Phe	Arg	Glu	Arg	Phe
														105
95														

Glu	Glu	Leu	Leu	Val	Phe	Val	Pro	His	Met	Arg	Arg	Phe	Leu	Ser
														120
110														

Arg	Lys	Lys	Ile	Arg	His	His	Ile	Tyr	Val	Leu	Asn	Gln	Val	Asp
														135
125														

His Phe Arg Phe Asn Arg Ala Ala Leu Ile Asn Val Gly Phe Leu

140	145	150
Glu Ser Ser Asn Ser Thr Asp Tyr Ile Ala Met His Asp Val Asp		
155	160	165
Leu Leu Pro Leu Asn Glu Glu Leu Asp Tyr Gly Phe Pro Glu Ala		
170	175	180
Gly Pro Phe His Val Ala Ser Pro Glu Leu His Pro Leu Tyr His		
185	190	195
Tyr Lys Thr Tyr Val Gly Gly Ile Leu Leu Leu Ser Lys Gln His		
200	205	210
Tyr Arg Leu Cys Asn Gly Met Ser Asn Arg Phe Trp Gly Trp Gly		
215	220	225
Arg Glu Asp Asp Glu Phe Tyr Arg Arg Ile Lys Gly Ala Gly Leu		
230	235	240
Gln Leu Phe Arg Pro Ser Gly Ile Thr Thr Gly Tyr Lys Thr Phe		
245	250	255
Arg His Leu His Asp Pro Ala Trp Arg Lys Arg Asp Gln Lys Arg		
260	265	270
Ile Ala Ala Gln Lys Gln Glu Gln Phe Lys Val Asp Arg Glu Gly		
275	280	285
Gly Leu Asn Thr Val Lys Tyr His Val Ala Ser Arg Thr Ala Leu		
290	295	300
Ser Val Gly Gly Ala Pro Cys Thr Val Leu Asn Ile Met Leu Asp		
305	310	315
Cys Asp Lys Thr Ala Thr Pro Trp Cys Thr Phe Ser		
320	325	

<210> 18

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 18

gcgaacgctt cgaggagtcc tgg 23

<210> 19

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24
<223> Synthetic construct

<400> 19
gcagtgcggg aagccacatg gtac 24

<210> 20
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 20
cttcctgagc aggaagaaga tccggcacca catctacgtg ctcaac 46

<210> 21
<211> 494
<212> DNA
<213> Homo sapiens

<400> 21
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aacgctgctg ctgctgctgc tgctgcttaa aggctcatgc ttggagtggg 100
gactggtcgg tgcccagaaa gtctttctg ccactgacgc ccccatcagg 150
gattggcct tctttcccccc ttcccttctg tgtctcctgc ctcatggcc 200
tgccatgacc tgcagccaag cccagccccc tgggaaaggg gagaaagtgg 250
gggatggcta agaaagctgg gagataggga acagaagagg gtagtgggtg 300
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atttatacaa agatattaag gccctgttca ttaagaaatt gttcccttcc 400
cctgtgttca atgttgtaa agattgttct gtgtaaatat gtcttataaa 450
taaacagttt aaagctgaaa aaaaaaaaaa aaaaaaaaaa aaaa 494

<210> 22
<211> 73
<212> PRT
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 1-15
<223> Signal peptide.

<220>
<221> misc_feature
<222> 3-18

<223> Growth factor and cytokines receptors family.

<400> 22

Met Leu Leu Leu Thr Leu Leu Leu Leu Leu Leu Lys Gly
1 5 10 15

Ser Cys Leu Glu Trp Gly Leu Val Gly Ala Gln Lys Val Ser Ser
20 25 30

Ala Thr Asp Ala Pro Ile Arg Asp Trp Ala Phe Phe Pro Pro Ser
35 40 45

Phe Leu Cys Leu Leu Pro His Arg Pro Ala Met Thr Cys Ser Gln
50 55 60

Ala Gln Pro Arg Gly Glu Gly Glu Lys Val Gly Asp Gly
65 70

<210> 23

<211> 2883

<212> DNA

<213> Homo sapiens

<400> 23

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ggctccgggg cggcccgcta ggccagtgcg ccgcgcgtcg cccgcaggc 200

cccgccccgc agcatgggc caccggacg ccggcgggc cgccgcgcgc 250

ccgcgttgtt gctgccgtc tcgctgttag cgctgctcgc gctgctggga 300

ggcggcgccg gcggcgccgc cgccgcgtc cccgcggct gcaagcacga 350

tggcgcccc cgaggggctg gcagggcgcc gggccccc gaggcaagg 400

tggtgtcag cagcctggaa ctcgcgcagg tcctcccccc agataactctg 450

cccaaccgca cggtcaccct gattctgagt aacaataaga tatccgagct 500

gaagaatggc tcatttctg ggttaagtct cttgaaaga ttggacacct 550

gaaaacaatct tattagtagt atagatccag gtgcctctg gggactgtca 600

tctctaaaaa gattggatct gacaaacaat cgaataggat gtctaatgc 650

agacatattt cgaggactca ccaatctggt tcggctaaac ctttcgggg 700

atttgttttc ttcattatct caaggaactt ttgattatct tgcgtcatta 750

cggctttgg aattccagac tgagtatctt ttgttgact gtaacataact 800

gtggatgcat cgctggtaa aggagaagaa catcacggta cgggatacca 850

ggtgtgttta tcctaagtca ctgcaggccc aaccagtcac aggcgtgaag 900
caggagctgt tgacatgcga ccctccgctt gaattgccgt ctttctacat 950
gactccatct catcgccaag ttgtgtttga aggagacagc cttccttcc 1000
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aaagagctag gtgacgtat ggttgcattt gcaagtaACA tcattgttGGC 1700
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catcaagtct actggcttca cggggatgac ctgtaccgtg ttccagaaaAG 1900
tggcagcCTC tgatcgtaCA ggactttcgG attatggag gcgggatCCA 1950
gagggaaACC tggataAGCA gctgagCTT aagtgcAAATG tttcaAAAtAC 2000
attttcgagt ctggcactAA aggtatgttA cattctgCAA tcatttaAGA 2050
ctatTTacAG ttaaattAGA atgctccAAA tggctctgCTT cgcaAAataAA 2100
ccttattAAAG agatTTTTT ttgcagGAAG ataggttATA ttgctttGC 2150
tactgtttta aagaaaaACTA accagGAAGA actgcattAC gactttCAAG 2200
ggcccttagGC atTTTGCCt ttgattccCT ttcttcacat AAAAATATCA 2250
gaaattACAT tttataACTG cagtggATA AATGCAAATA tactattgtt 2300

acatgtgaaa aaattttatt tgacttaaaa gtttatttat ttgtttttt 2350
gctcctgatt ttaagacaat aagatgttt catggccccc taaaagtatc 2400
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acacaaatat gtcataatc ttttttaaa aaaagtatcc cattgaagca 2550
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tcaataatat cacaaacaat attccagtc tttaatggc tgcataataa 2800
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<210> 24
<211> 616
<212> PRT
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 1-33
<223> Signal peptide.

<220>
<221> TRANSMEM
<222> 13-40
<223> Transmembrane domain (type II).

<400> 24
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20 25 30
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35 40 45
Asp Gly Arg Pro Arg Gly Ala Gly Arg Ala Ala Gly Ala Ala Glu
50 55 60
Gly Lys Val Val Cys Ser Ser Leu Glu Leu Ala Gln Val Leu Pro
65 70 75
Pro Asp Thr Leu Pro Asn Arg Thr Val Thr Leu Ile Leu Ser Asn
80 85 90

Asn Lys Ile Ser Glu Leu Lys Asn Gly Ser Phe Ser Gly Leu Ser
 95 100 105
 Leu Leu Glu Arg Leu Asp Leu Arg Asn Asn Leu Ile Ser Ser Ile
 110 115 120
 Asp Pro Gly Ala Phe Trp Gly Leu Ser Ser Leu Lys Arg Leu Asp
 125 130 135
 Leu Thr Asn Asn Arg Ile Gly Cys Leu Asn Ala Asp Ile Phe Arg
 140 145 150
 Gly Leu Thr Asn Leu Val Arg Leu Asn Leu Ser Gly Asn Leu Phe
 155 160 165
 Ser Ser Leu Ser Gln Gly Thr Phe Asp Tyr Leu Ala Ser Leu Arg
 170 175 180
 Ser Leu Glu Phe Gln Thr Glu Tyr Leu Leu Cys Asp Cys Asn Ile
 185 190 195
 Leu Trp Met His Arg Trp Val Lys Glu Lys Asn Ile Thr Val Arg
 200 205 210
 Asp Thr Arg Cys Val Tyr Pro Lys Ser Leu Gln Ala Gln Pro Val
 215 220 225
 Thr Gly Val Lys Gln Glu Leu Leu Thr Cys Asp Pro Pro Leu Glu
 230 235 240
 Leu Pro Ser Phe Tyr Met Thr Pro Ser His Arg Gln Val Val Phe
 245 250 255
 Glu Gly Asp Ser Leu Pro Phe Gln Cys Met Ala Ser Tyr Ile Asp
 260 265 270
 Gln Asp Met Gln Val Leu Trp Tyr Gln Asp Gly Arg Ile Val Glu
 275 280 285
 Thr Asp Glu Ser Gln Gly Ile Phe Val Glu Lys Asn Met Ile His
 290 295 300
 Asn Cys Ser Leu Ile Ala Ser Ala Leu Thr Ile Ser Asn Ile Gln
 305 310 315
 Ala Gly Ser Thr Gly Asn Trp Gly Cys His Val Gln Thr Lys Arg
 320 325 330
 Gly Asn Asn Thr Arg Thr Val Asp Ile Val Val Leu Glu Ser Ser
 335 340 345
 Ala Gln Tyr Cys Pro Pro Glu Arg Val Val Asn Asn Lys Gly Asp
 350 355 360
 Phe Arg Trp Pro Arg Thr Leu Ala Gly Ile Thr Ala Tyr Leu Gln
 365 370 375
 Cys Thr Arg Asn Thr His Gly Ser Gly Ile Tyr Pro Gly Asn Pro

380	385	390
Gln Asp Glu Arg Lys Ala Trp Arg Arg Cys Asp Arg Gly Gly Phe		
395	400	405
Trp Ala Asp Asp Asp Tyr Ser Arg Cys Gln Tyr Ala Asn Asp Val		
410	415	420
Thr Arg Val Leu Tyr Met Phe Asn Gln Met Pro Leu Asn Leu Thr		
425	430	435
Asn Ala Val Ala Thr Ala Arg Gln Leu Leu Ala Tyr Thr Val Glu		
440	445	450
Ala Ala Asn Phe Ser Asp Lys Met Asp Val Ile Phe Val Ala Glu		
455	460	465
Met Ile Glu Lys Phe Gly Arg Phe Thr Lys Glu Glu Lys Ser Lys		
470	475	480
Glu Leu Gly Asp Val Met Val Asp Ile Ala Ser Asn Ile Met Leu		
485	490	495
Ala Asp Glu Arg Val Leu Trp Leu Ala Gln Arg Glu Ala Lys Ala		
500	505	510
Cys Ser Arg Ile Val Gln Cys Leu Gln Arg Ile Ala Thr Tyr Arg		
515	520	525
Leu Ala Gly Gly Ala His Val Tyr Ser Thr Tyr Ser Pro Asn Ile		
530	535	540
Ala Leu Glu Ala Tyr Val Ile Lys Ser Thr Gly Phe Thr Gly Met		
545	550	555
Thr Cys Thr Val Phe Gln Lys Val Ala Ala Ser Asp Arg Thr Gly		
560	565	570
Leu Ser Asp Tyr Gly Arg Arg Asp Pro Glu Gly Asn Leu Asp Lys		
575	580	585
Gln Leu Ser Phe Lys Cys Asn Val Ser Asn Thr Phe Ser Ser Leu		
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Ser		

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 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24

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<223> Synthetic construct

<400> 25
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<210> 26
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 26
aactggaaag gaaggctgtc tccc 24

<210> 27
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 27
gtaaaggaga agaacatcac ggtacggat accaggtgtg tttatcctaa 50

<210> 28
<211> 683
<212> DNA
<213> Homo sapiens

<400> 28
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gcagaggctt cgtgacggag ttatcagaga cattgagagg caaattcgg 150
aaaaagaaaa cattcgtctt ttgggagaac agattatttt gactgagcaa 200
cttgaagcag aaagagagaa gatgttattt gcaaaaaggat ctcaaaaatc 250
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ctgctttcag ggtcccttat atctgaataa aggagtgtgg gcagacactt 450
tttggaaagag tctgtctggg tgatcctggt agaagccccca ttagggcac 500
tgtccagtgcc ttagggttgt tactgagaag cactgccgag cttgtgagaa 550

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ggaagggatg gatacttagca tccacctgag tagtctgatc agtcggcatg 600
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 gtggagggag agacgctcct gatcgctgaa tcc 683

 <210> 29
 <211> 81
 <212> PRT
 <213> Homo sapiens

 <220>
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 <222> 1-21
 <223> Signal peptide.

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 Gln Gln Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln
 35 40 45

 Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile
 50 55 60

 Leu Thr Glu Gln Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala
 65 70 75

 Lys Gly Ser Gln Lys Ser
 80

<210> 30
 <211> 2128
 <212> DNA
 <213> Homo sapiens

<400> 30
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 tccgtggatt cctctgctaa gaccgctgcc atgccagtga cggtaacccg 150
 caccaccatc acaaccacca cgacgtcatc ttccggcctg gggccccca 200
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 gggccctgg acggggtcca tgggcaactg gtccatgttc acctggtgct 350
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ctatgcggcc ctcttctgcc tctcggccctc catcatctac cccaccacct 500
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 <210> 31
 <211> 322
 <212> PRT
 <213> Homo sapiens

 <400> 31
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 35 40 45
 Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp
 50 55 60
 Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys
 65 70 75
 Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu
 80 85 90
 Gln Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe
 95 100 105
 Ala Cys Tyr Ala Ala Leu Phe Cys Leu Ser Ala Ser Ile Ile Tyr
 110 115 120
 Pro Thr Thr Tyr Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp
 125 130 135
 His Ala Ile Ala Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala
 140 145 150
 Tyr Ala Thr Glu Val Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile
 155 160 165
 Thr Gly Tyr Met Ala Thr Val Pro Gly Leu Leu Lys Val Leu Glu
 170 175 180
 Thr Phe Val Ala Cys Ile Ile Phe Ala Phe Ile Ser Asp Pro Asn
 185 190 195
 Leu Tyr Gln His Gln Pro Ala Leu Glu Trp Cys Val Ala Val Tyr
 200 205 210

Ala Ile Cys Phe Ile Leu Ala Ala Ile Ala Ile Leu Leu Asn Leu
 215 220 225
 Gly Glu Cys Thr Asn Val Leu Pro Ile Pro Phe Pro Ser Phe Leu
 230 235 240
 Ser Gly Leu Ala Leu Leu Ser Val Leu Leu Tyr Ala Thr Ala Leu
 245 250 255
 Val Leu Trp Pro Leu Tyr Gln Phe Asp Glu Lys Tyr Gly Gly Gln
 260 265 270
 Pro Arg Arg Ser Arg Asp Val Ser Cys Ser Arg Ser His Ala Tyr
 275 280 285
 Tyr Val Cys Ala Trp Asp Arg Arg Leu Ala Val Ala Ile Leu Thr
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 Ala Ile Asn Leu Leu Ala Tyr Val Ala Asp Leu Val His Ser Ala
 305 310 315
 His Leu Val Phe Val Lys Val
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<210> 32
 <211> 3680
 <212> DNA
 <213> Homo sapiens

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 ctggccagcc tatgcatttt taagaaattt ttctgttata ggtgctgtgc 200
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 <212> PRT
 <213> Homo sapiens
 <400> 33
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 20 25 30
 Ser Leu Ala Gln Val Asn Leu Ser Pro Phe Ser His Pro Lys Val
 35 40 45
 His Met Asp Pro Asn Tyr Cys His Pro Ser Thr Ser Leu His Leu
 50 55 60
 Cys Ser Leu Ala Trp Ser Phe Thr Arg Leu Leu His Pro Pro Leu
 65 70 75
 Ser Pro Gly Ile Ser Gln Val Val Lys Asp His Val Thr Lys Pro
 80 85 90
 Thr Ala Met Ala Gln Gly Arg Val Ala His Leu Ile Glu Trp Lys
 95 100 105
 Gly Trp Ser Lys Pro Ser Asp Ser Pro Ala Ala Leu Glu Ser Ala
 110 115 120
 Phe Ser Ser Tyr Ser Asp Leu Ser Glu Gly Glu Gln Glu Ala Arg
 125 130 135
 Phe Ala Ala Gly Val Ala Glu Gln Phe Ala Ile Ala Glu Ala Lys
 140 145 150
 Leu Arg Ala Trp Ser Ser Val Asp Gly Glu Asp Ser Thr Asp Asp
 155 160 165
 Ser Tyr Asp Glu Asp Phe Ala Gly Gly Met Asp Thr Asp Met Ala
 170 175 180
 Gly Gln Leu Pro Leu Gly Pro His Leu Gln Asp Leu Phe Thr Gly
 185 190 195
 His Arg Phe Ser Arg Pro Val Arg Gln Gly Ser Val Glu Pro Glu
 200 205 210
 Ser Asp Cys Ser Gln Thr Val Ser Pro Asp Thr Leu Cys Ser Ser
 215 220 225
 Leu Cys Ser Leu Glu Asp Gly Leu Leu Gly Ser Pro Ala Arg Leu
 230 235 240

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Ala Ser Gln Leu Leu Gly Asp Glu Leu Leu Leu Ala Lys Leu Pro
245           250           255
Pro Ser Arg Glu Ser Ala Phe Arg Ser Leu Gly Pro Leu Glu Ala
260           265           270
Gln Asp Ser Leu Tyr Asn Ser Pro Leu Thr Glu Ser Cys Leu Ser
275           280           285
Pro Ala Glu Glu Glu Pro Ala Pro Cys Lys Asp Cys Gln Pro Leu
290           295           300
Cys Pro Pro Leu Thr Gly Ser Trp Glu Arg Gln Arg Gln Ala Ser
305           310           315
Asp Leu Ala Ser Ser Gly Val Val Ser Leu Asp Glu Asp Glu Ala
320           325           330
Glu Pro Glu Glu Gln
335

<210> 34
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct

<400> 34
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<210> 35
<211> 50
<212> DNA
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<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 35
ctggatgcta atgtgtccag taaatgatcc ccttatcccg tcgcgatgct 50

<210> 36
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 36

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ttccactcaa tgaggtgagc cactc 25

<210> 37
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-23
<223> Synthetic construct.

<400> 37
ggcgagccct aactatccag gag 23

<210> 38
<211> 39
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-39
<223> Synthetic construct.

<400> 38
ggagatcgct gcgctggcca ggtcctccct gcatggat 39

<210> 39
<211> 22
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-22
<223> Synthetic construct.

<400> 39
ctgctgcaaa gcgagcctct tg 22

<210> 40
<211> 2084
<212> DNA
<213> Homo sapiens

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ccatctgttt tctctaattgc acgacagatt cctttcagac aggacaactg 150

tgatatttca gttcctgatt gtaaataacct cctaaggctg aagcttctgt 200

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caatcttattc ttgccacatc aagggattgt tattccttta aaaaaaaaaacc 300

aataccaaag aaggctacaa tggcgttttgc agccaaaatt ctgttgattt 350
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gacataaaaca caacacagaa cattgcagaa gtttttaaaa caatggaaaa 450
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gatgaagatc ttttgcccat ctcagcacat cccaaatgcta cacctgctct 750
gtcttcagaa aacttcactt ggtctttgggt caatgacacc gtgaaaactc 800
ctgataacag ttccattaca gtttagcatcc tctcttcaga accaacttct 850
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cagtgatagc ttcaactgggt ttacccctta tcaagaaaaa acaactctac 950
agcctacctt aaaattcacc aataattcaa aactctttcc aaatacgtca 1000
gatccccaaa aagaaaaatag aaatacagga atagtattcg gggccatttt 1050
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tgtatTTAG tagtattttc ttagtagaaaa atattgtgg aatcagataaa 1600
aactaaaaaga ttccaccatt acagccctgc ctcataacta aataataaaa 1650
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catagccag agtttctgtt attggaaat tgaggcaata gaaatgacag 1850
acctgtattc tagtacgtta taatttcta gatcagcaca cacatgatca 1900
gcccaactgag ttatgaagct gacaatgact gcattcaacg gggccatggc 1950
aggaaagctg accctaccca ggaaagtaat agcttcttta aaagtcttca 2000
aaggtttgg gaatttaac ttgtcttaat atatcttagg cttcaattat 2050
ttgggtgcct taaaaactca atgagaatca tggt 2084

<210> 41
<211> 334
<212> PRT
<213> Homo sapiens

<400> 41
Met Leu Ala Leu Ala Lys Ile Leu Leu Ile Ser Thr Leu Phe Tyr
1 5 10 15

Ser Leu Leu Ser Gly Ser His Gly Lys Glu Asn Gln Asp Ile Asn
20 25 30

Thr Thr Gln Asn Ile Ala Glu Val Phe Lys Thr Met Glu Asn Lys
35 40 45

Pro Ile Ser Leu Glu Ser Glu Ala Asn Leu Asn Ser Asp Lys Glu
50 55 60

Asn Ile Thr Thr Ser Asn Leu Lys Ala Ser His Ser Pro Pro Leu
65 70 75

Asn Leu Pro Asn Asn Ser His Gly Ile Thr Asp Phe Ser Ser Asn
80 85 90

Ser Ser Ala Glu His Ser Leu Gly Ser Leu Lys Pro Thr Ser Thr
95 100 105

Ile Ser Thr Ser Pro Pro Leu Ile His Ser Phe Val Ser Lys Val
110 115 120

Pro Trp Asn Ala Pro Ile Ala Asp Glu Asp Leu Leu Pro Ile Ser
125 130 135

Ala His Pro Asn Ala Thr Pro Ala Leu Ser Ser Glu Asn Phe Thr
140 145 150

Trp Ser Leu Val Asn Asp Thr Val Lys Thr Pro Asp Asn Ser Ser
155 160 165

Ile Thr Val Ser Ile Leu Ser Ser Glu Pro Thr Ser Pro Ser Val
170 175 180

Thr Pro Leu Ile Val Glu Pro Ser Gly Trp Leu Thr Thr Asn Ser
185 190 195

Asp Ser Phe Thr Gly Phe Thr Pro Tyr Gln Glu Lys Thr Thr Leu
 200 205 210
 Gln Pro Thr Leu Lys Phe Thr Asn Asn Ser Lys Leu Phe Pro Asn
 215 220 225
 Thr Ser Asp Pro Gln Lys Glu Asn Arg Asn Thr Gly Ile Val Phe
 230 235 240
 Gly Ala Ile Leu Gly Ala Ile Leu Gly Val Ser Leu Leu Thr Leu
 245 250 255
 Val Gly Tyr Leu Leu Cys Gly Lys Arg Lys Thr Asp Ser Phe Ser
 260 265 270
 His Arg Arg Leu Tyr Asp Asp Arg Asn Glu Pro Val Leu Arg Leu
 275 280 285
 Asp Asn Ala Pro Glu Pro Tyr Asp Val Ser Phe Gly Asn Ser Ser
 290 295 300
 Tyr Tyr Asn Pro Thr Leu Asn Asp Ser Ala Met Pro Glu Ser Glu
 305 310 315
 Glu Asn Ala Arg Asp Gly Ile Pro Met Asp Asp Ile Pro Pro Leu
 320 325 330
 Arg Thr Ser Val

<210> 42
 <211> 1594
 <212> DNA
 <213> Homo sapiens

<400> 42
 aacaggatct cctttgcag tctgcagccc aggacgctga ttccagcagc 50
 gccttaccgc gcagcccgaa gattcactat ggtaaaaatc gccttcaata 100
 cccctaccgc cgtcaaaag gaggaggcgc ggcaaga<gt> ggaggccctc 150
 ctgagccgca cggtcagaac tcagatactg accggcaagg agctccgagt 200
 tgccacccag gaaaaagagg gtcctctgg gagatgtatg cttactct 250
 taggccttgc attcatcttgcaggactta ttgttggtgg agcctgcatt 300
 tacaagtact tcatgccaa gagcaccatt taccgtggag agatgtgctt 350
 ttttGattct gaggatcctg caaattccct tcgtggagga gagcctaact 400
 tcctgcctgt gactgaggag gctgacattc gtgaggatga caacattgca 450
 atcattgatg tgcctgtccc cagttctct gatagtgacc ctgcagcaat 500
 tattcatgac tttgaaaagg gaatgactgc ttacctggac ttgttgctgg 550

ggaactgcta tctgatgccc ctcaatactt ctattgttat gcctccaaaa 600
aatctggtag agctcttgg caaactggcg agtggcagat atctgcctca 650
aacttatgtg gttcgagaag acctagttgc tgtggaggaa attcgtgatg 700
ttagtaacct tggcatctt atttaccaac tttgcaataa cagaaagtcc 750
ttccgccttc gtgcagaga cctcttgctg ggttcaaca aacgtgccat 800
tgataaatgc tggaaagatta gacacttccc caacgaattt attgttgaga 850
ccaagatctg tcaagagtaa gaggcaacag atagagtgtc cttggtaata 900
agaagtca gatttacaat atgactttaa cattaagggtt tatgggatac 950
tcaagatatt tactcatgca ttactctat tgcttatgct taaaaaaaaag 1000
gaaaaaaaaaaa aaaactacta accactgcaa gctcttgtca aatttttagtt 1050
taattggcat tgcttgaaaa ttgaaactga aattacatga gtttcatttt 1100
ttctttgcat ttatagggtt tagatttctg aaagcagcat gaatatatca 1150
cctaacatcc tgacaataaa ttccatccgt tgaaaaaaa gtttgggtgt 1200
tttttctttt ccttaagta agctctttat tcattttatg gtggagcaat 1250
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tatcagatct caacattgtt ggtttctttt gtttttcatt ttgtacaact 1350
ttcttgaatt tagaaattac atctttgcag ttctgttagg tgctctgtaa 1400
ttaacctgac ttatatgtga acaattttca tgagacagtc atttttact 1450
aatgcagtga ttctttctca ctactatctg tattgtggaa tgcacaaaaat 1500
tgtgttaggtg ctgaatgctg taaggagttt aggttgtatg aattctacaa 1550
ccctataata aattttactc tataaaaaaa aaaaaaaaaaaa aaaa 1594

<210> 43
<211> 263
<212> PRT
<213> Homo sapiens

<400> 43
Met Val Lys Ile Ala Phe Asn Thr Pro Thr Ala Val Gln Lys Glu
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Glu Ala Arg Gln Asp Val Glu Ala Leu Leu Ser Arg Thr Val Arg
20 25 30
Thr Gln Ile Leu Thr Gly Lys Glu Leu Arg Val Ala Thr Gln Glu
35 40 45
Lys Glu Gly Ser Ser Gly Arg Cys Met Leu Thr Leu Leu Gly Leu

50	55	60
Ser Phe Ile Leu Ala Gly Leu Ile Val Gly Gly Ala Cys Ile Tyr		
65	70	75
Lys Tyr Phe Met Pro Lys Ser Thr Ile Tyr Arg Gly Glu Met Cys		
80	85	90
Phe Phe Asp Ser Glu Asp Pro Ala Asn Ser Leu Arg Gly Gly Glu		
95	100	105
Pro Asn Phe Leu Pro Val Thr Glu Glu Ala Asp Ile Arg Glu Asp		
110	115	120
Asp Asn Ile Ala Ile Ile Asp Val Pro Val Pro Ser Phe Ser Asp		
125	130	135
Ser Asp Pro Ala Ala Ile Ile His Asp Phe Glu Lys Gly Met Thr		
140	145	150
Ala Tyr Leu Asp Leu Leu Leu Gly Asn Cys Tyr Leu Met Pro Leu		
155	160	165
Asn Thr Ser Ile Val Met Pro Pro Lys Asn Leu Val Glu Leu Phe		
170	175	180
Gly Lys Leu Ala Ser Gly Arg Tyr Leu Pro Gln Thr Tyr Val Val		
185	190	195
Arg Glu Asp Leu Val Ala Val Glu Glu Ile Arg Asp Val Ser Asn		
200	205	210
Leu Gly Ile Phe Ile Tyr Gln Leu Cys Asn Asn Arg Lys Ser Phe		
215	220	225
Arg Leu Arg Arg Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala		
230	235	240
Ile Asp Lys Cys Trp Lys Ile Arg His Phe Pro Asn Glu Phe Ile		
245	250	255
Val Glu Thr Lys Ile Cys Gln Glu		
260		

<210> 44
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-24
<223> Synthetic construct.

<400> 44
gaaagacacg acacagcagc ttgc 24

<210> 45

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<211> 20
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-20
<223> Synthetic construct.

<400> 45
gffaactgct atctgatgcc 20

<210> 46
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-26
<223> Synthetic construct.

<400> 46
caggatctcc tcttgagtc tgcagc 26

<210> 47
<211> 28
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-28
<223> Synthetic construct.

<400> 47
cttctcgAAC cacataagtt tgagggAG 28

<210> 48
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 48
cacgattccc tccacagcaa ctggg 25

<210> 49
<211> 1969
<212> DNA
<213> Homo sapiens

<400> 49
ggaggaggga gggcgggcag gcGCCAGCCC agAGCAGCCC CGGGCACCAg 50
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cgggagcacc cagtcctgtat cgccaaggaa ctgggcctgg gggcaccatg 150
gtttcggcgg cagcccccaag cctcctcatc cttctgttgc tgctgctggg 200
gtctgtgcct gctaccgcacg cccgctctgt gcccctgaag gccacgttcc 250
tggaggatgt ggcgggtagt ggggaggccg agggctcgac ggcctcctcc 300
ccgagcctcc cgccaccctg gaccccgccc ctcagccca catcgatggg 350
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atgggatagt ggacttcttc cgccagtaac tgatgtctat tgctgtggg 450
ggctccctgg ccttctgtat gatgttcatc gtctgtgccg cggtcatcac 500
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ctcccgccag ctccaggccc acatcttggc cgccaccctg aacctaagt 700
cccccaccag ggctgcactg ggcgggtgggg acggagccag gatggtgag 750
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cagaaaaatgt ggtccccggt gccccggagg aatcttacca agtgcacca 1200
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ccccccaaatgt gctgggatta caggcgtgag ccaccgtgcc cggcccaaac 1350
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caagcacccc cgccctgggg gtgagttct catcccgcta ctgctgctgg 1550
gatcagggtt aatgaatgga actcttcctg tctggcctcc aaagcagcct 1600
agaagctgag gggctgtt tgaggggacc tccaccctgg ggaagtccga 1650
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gtcagtcctc gacagggagc ctgggctccg tcctgcttta gggaggctct 1800
ggcaggaggt cctctcccc atccctccat ctggggctcc cccaacctct 1850
gcacagctct ccaggtgctg agatataatg caccagcaca ataaaccttt 1900
attccggcct gaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa 1950
aaaaaaaaaaa aaaaaaaga 1969

<210> 50
<211> 283
<212> PRT
<213> Homo sapiens

<400> 50
 Met Val Ser Ala Ala Ala Pro Ser Leu Leu Ile Leu Leu Leu Leu
 1 5 10 15
 Leu Leu Gly Ser Val Pro Ala Thr Asp Ala Arg Ser Val Pro Leu
 20 25 30
 Lys Ala Thr Phe Leu Glu Asp Val Ala Gly Ser Gly Glu Ala Glu
 35 40 45
 Gly Ser Ser Ala Ser Ser Pro Ser Leu Pro Pro Pro Trp Thr Pro
 50 55 60
 Ala Leu Ser Pro Thr Ser Met Gly Pro Gln Pro Thr Thr Leu Gly
 65 70 75
 Gly Pro Ser Pro Pro Thr Asn Phe Leu Asp Gly Ile Val Asp Phe
 80 85 90
 Phe Arg Gln Tyr Val Met Leu Ile Ala Val Val Gly Ser Leu Ala
 95 100 105
 Phe Leu Leu Met Phe Ile Val Cys Ala Ala Val Ile Thr Arg Gln
 110 115 120
 Lys Gln Lys Ala Ser Ala Tyr Tyr Pro Ser Ser Phe Pro Lys Lys
 125 130 135
 Lys Tyr Val Asp Gln Ser Asp Arg Ala Gly Gly Pro Arg Ala Phe
 140 145 150
 Ser Glu Val Pro Asp Arg Ala Pro Asp Ser Arg Pro Glu Glu Ala
 155 160 165

Leu	Asp	Ser	Ser	Arg	Gln	Leu	Gln	Ala	Asp	Ile	Leu	Ala	Ala	Thr
170									175					180
Gln	Asn	Leu	Lys	Ser	Pro	Thr	Arg	Ala	Ala	Leu	Gly	Gly	Gly	Asp
185									190					195
Gly	Ala	Arg	Met	Val	Glu	Gly	Arg	Gly	Ala	Glu	Glu	Glu	Glu	Lys
200									205					210
Gly	Ser	Gln	Glu	Gly	Asp	Gln	Glu	Val	Gln	Gly	His	Gly	Val	Pro
215									220					225
Val	Glu	Thr	Pro	Glu	Ala	Gln	Glu	Glu	Pro	Cys	Ser	Gly	Val	Leu
230									235					240
Glu	Gly	Ala	Val	Val	Ala	Gly	Glu	Gly	Gln	Gly	Glu	Leu	Glu	Gly
245									250					255
Ser	Leu	Leu	Leu	Ala	Gln	Glu	Ala	Gln	Gly	Pro	Val	Gly	Pro	Pro
260									265					270
Glu	Ser	Pro	Cys	Ala	Cys	Ser	Ser	Val	His	Pro	Ser	Val		
275									280					

<210> 51
 <211> 1734
 <212> DNA
 <213> Homo sapiens

<400> 51
 gtggactctg agaagccag gcagttgagg acaggagaga gaaggctgca 50
 gacccagagg gagggaggac agggagtcgg aaggaggagg acagaggagg 100
 gcacagagac gcagagcaag ggcggcaagg aggagaccct ggtggagga 150
 agacactctg gagagagagg gggctggca gagatgaagt tccagggcc 200
 cctggcctgc ctcctgctgg ccctctgcct gggcagtggg gaggctggcc 250
 ccctgcagag cggagaggaa agcactggaa caaatatgg ggaggccctt 300
 ggacatggcc tggagacgc cctgagcgaa ggggtggaa aggccattgg 350
 caaagaggcc ggagggcag ctggctctaa agtcatgtag gcccttgccc 400
 aagggaccag agaagcagtt ggcactggag tcaggcaggt tccaggcttt 450
 ggcgcagcag atgctttggg caacagggtc ggggaagcag cccatgctct 500
 gggaaacact gggcacgaga ttggcagaca ggcagaagat gtcattcgac 550
 acggagcaga tgctgtccgc ggctcctggc agggggtgcc tggccacagt 600
 ggtgcttggg aaacttctgg aggccatggc atcttggct ctcaaggtagg 650
 ccttggagggc cagggccagg gcaatcctgg aggtctgggg actccgtggg 700

tccacggata ccccgaaac tcagcaggca gctttgaat gaatcctcag 750
ggagctccct ggggtcaagg aggcaatgga gggccaccaa actttggac 800
caacactcag ggagctgtgg cccagcctgg ctatggtca gtgagagcca 850
gcaaccagaa tgaagggtgc acgaatcccc caccatctgg ctcaggtgga 900
ggctccagca actctgggg aggcaagcgc tcacagtgg gcagcagtgg 950
cagtggcagc aatggtgaca acaacaatgg cagcagcagt ggtggcagca 1000
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tgagtcctcc tgggatcca gcaccggctc ctcctccggc aaccacggtg 1150
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gaagcccgcg ggagcgggga atctgggatt cagggctca gaggacaggg 1250
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ggaggtgacg ctgttgtgg agtcaatact gtgaactctg agacgtctcc 1400
tggatgttt aactttgaca ctttctggaa gaattttaaa tccaagctgg 1450
gtttcatcaa ctggatgcc ataaacaagg accagagaag ctctcgcatc 1500
ccgtgaccc cagacaagga gccaccagat tggatggag ccccccacact 1550
ccctccttaa aacaccaccc tctcatcact aatctcagcc cttgcccttg 1600
aaataaacct tagctgcccc aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1650
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1700
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1734

<210> 52
<211> 440
<212> PRT
<213> Homo sapiens

<400> 52
Met Lys Phe Gln Gly Pro Leu Ala Cys Leu Leu Leu Ala Leu Cys
1 5 10 15
Leu Gly Ser Gly Glu Ala Gly Pro Leu Gln Ser Gly Glu Glu Ser
20 25 30
Thr Gly Thr Asn Ile Gly Glu Ala Leu Gly His Gly Leu Gly Asp
35 40 45
Ala Leu Ser Glu Gly Val Gly Lys Ala Ile Gly Lys Glu Ala Gly

50	55	60
Gly Ala Ala Gly Ser Lys Val Ser Glu Ala Leu Gly Gln Gly Thr		
65	70	75
Arg Glu Ala Val Gly Thr Gly Val Arg Gln Val Pro Gly Phe Gly		
80	85	90
Ala Ala Asp Ala Leu Gly Asn Arg Val Gly Glu Ala Ala His Ala		
95	100	105
Leu Gly Asn Thr Gly His Glu Ile Gly Arg Gln Ala Glu Asp Val		
110	115	120
Ile Arg His Gly Ala Asp Ala Val Arg Gly Ser Trp Gln Gly Val		
125	130	135
Pro Gly His Ser Gly Ala Trp Glu Thr Ser Gly Gly His Gly Ile		
140	145	150
Phe Gly Ser Gln Gly Gly Leu Gly Gly Gln Gly Gln Gly Asn Pro		
155	160	165
Gly Gly Leu Gly Thr Pro Trp Val His Gly Tyr Pro Gly Asn Ser		
170	175	180
Ala Gly Ser Phe Gly Met Asn Pro Gln Gly Ala Pro Trp Gly Gln		
185	190	195
Gly Gly Asn Gly Gly Pro Pro Asn Phe Gly Thr Asn Thr Gln Gly		
200	205	210
Ala Val Ala Gln Pro Gly Tyr Gly Ser Val Arg Ala Ser Asn Gln		
215	220	225
Asn Glu Gly Cys Thr Asn Pro Pro Pro Ser Gly Ser Gly Gly Gly		
230	235	240
Ser Ser Asn Ser Gly Gly Ser Gly Ser Gln Ser Gly Ser Ser		
245	250	255
Gly Ser Gly Ser Asn Gly Asp Asn Asn Asn Gly Ser Ser Ser Gly		
260	265	270
Gly Ser Ser Ser Gly Ser Ser Ser Gly Ser Ser Ser Gly Gly Ser		
275	280	285
Ser Gly Gly Ser Ser Gly Ser Ser Gly Asn Ser Gly Gly Ser		
290	295	300
Arg Gly Asp Ser Gly Ser Glu Ser Ser Trp Gly Ser Ser Thr Gly		
305	310	315
Ser Ser Ser Gly Asn His Gly Gly Ser Gly Gly Asn Gly His		
320	325	330
Lys Pro Gly Cys Glu Lys Pro Gly Asn Glu Ala Arg Gly Ser Gly		
335	340	345

Glu	Ser	Gly	Ile	Gln	Gly	Phe	Arg	Gly	Gln	Gly	Val	Ser	Ser	Asn
														350
														355
														360
Met	Arg	Glu	Ile	Ser	Lys	Glu	Gly	Asn	Arg	Leu	Leu	Gly	Gly	Ser
														365
														370
														375
Gly	Asp	Asn	Tyr	Arg	Gly	Gln	Gly	Ser	Ser	Trp	Gly	Ser	Gly	Gly
														380
														385
														390
Gly	Asp	Ala	Val	Gly	Gly	Val	Asn	Thr	Val	Asn	Ser	Glu	Thr	Ser
														395
														400
														405
Pro	Gly	Met	Phe	Asn	Phe	Asp	Thr	Phe	Trp	Lys	Asn	Phe	Lys	Ser
														410
														415
														420
Lys	Leu	Gly	Phe	Ile	Asn	Trp	Asp	Ala	Ile	Asn	Lys	Asp	Gln	Arg
														425
														430
Ser	Ser	Arg	Ile	Pro										
														440

<210> 53

<211> 3580

<212> DNA

<213> Homo sapiens

<400> 53

gaccgggtccc	tccggtcctg	gatgtgcgga	ctctgctgca	gcgaggggctg	50
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ctttgctgac	catgttgttc	ccttgctgga	atattaccgg	gacatcttca	150
ctctcctgct	gcccctgcac	cggagcttg	tgttgtcgca	ggagagttag	200
ggaaagatgt	gtttcctgaa	caagctgctg	ctacttgctg	tcctgggctg	250
gctttccag	attcccacag	tccctgagga	cttggttctt	ctggaagagg	300
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gacggagtgg	ggggttcatg	aggaaaatca	ccccaccac	taccaccagc	500
ctgggagccc	agccttccca	gaccagccag	gggctgcagg	cacagctcgc	550
ccaggccctt	ttccacaacc	agccgccc	cttgcgcgg	accgttagtg	600
tcgtggcaga	aagaatttgg	tcaaacttg	tcaaacatat	caaggctaca	650
ctgggtggcag	atctggtgcg	ccaggcagag	tcaacttctcc	aagagcagct	700
ggtgacacag	ggagaggaag	ggggagaccc	agcccagctg	ttggagatct	750
tgtgttccca	gctgtgcct	cacggggccc	aggcattggc	cctggggcgg	800

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ttgcaacaga gaaaggctgt gcttggctgt cagccaacat cacagcactg 950
atcaggaggg aggtgaaagc agcagtgagt cgcacacttc gagcccaggg 1000
tcctgaacct gctgcccggg gggagcggag gggctgctcc cgccctgac 1050
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gccagttcct gtgcccacct gctgagcagc atctggcaaa gtgctctgt 1200
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<212> PRT
<213> Homo sapiens

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 35 40 45
 His Gly Leu Asp Asn Ala Pro Val Val Asp Gln Gln Leu Leu Tyr
 50 55 60
 Thr Cys Cys Pro Tyr Ile Gly Glu Leu Arg Lys Leu Leu Ala Ser
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 Ile Thr Pro Thr Thr Ser Leu Gly Ala Gln Pro Ser Gln
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 Asn Gln Pro Pro Ser Leu Arg Arg Thr Val Glu Phe Val Ala Glu
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 170 175 180
 Ile Leu Cys Ser Gln Leu Cys Pro His Gly Ala Gln Ala Leu Ala
 185 190 195
 Leu Gly Arg Glu Phe Cys Gln Arg Lys Ser Pro Gly Ala Val Arg
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 Ala Leu Leu Pro Glu Glu Thr Pro Ala Ala Val Leu Ser Ser Ala
 215 220 225
 Glu Asn Ile Ala Val Gly Leu Ala Thr Glu Lys Ala Cys Ala Trp
 230 235 240
 Leu Ser Ala Asn Ile Thr Ala Leu Ile Arg Arg Glu Val Lys Ala
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<212> DNA
<213> Homo sapiens

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<211> 299
<212> PRT
<213> Homo sapiens

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<211> 4277

<212> DNA

<213> Homo sapiens

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<211> 1115

<212> PRT

<213> Homo sapiens

<400> 58

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Cys	Val	Ala	Arg	Met	Pro	Ala	Gly	Ala	Val	Ala	Ser	Val	Pro	Ala
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 350 355 360
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 Ala Glu Leu Ala Thr Gly Thr Pro Pro Val Ser Pro Ser Lys Leu
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 Gly Asn Pro Glu Gln Met Leu Arg Gly Gln Pro Ala Leu Pro Arg
 440 445 450
 Pro Pro Thr Ser Val Gly Pro Ala Ser Pro Lys Cys Pro Gly Glu
 455 460 465
 Lys Gly Gln Gly Ala Pro Ala Glu Ala Pro Ile Ile Leu Ser Ser
 470 475 480
 Pro Arg Thr Ser Lys Thr Asp Ser Tyr Glu Leu Val Trp Arg Pro
 485 490 495
 Arg His Glu Gly Ser Gly Arg Ala Pro Ile Leu Tyr Tyr Val Val
 500 505 510
 Lys His Arg Lys Gln Val Thr Asn Ser Ser Asp Asp Trp Thr Ile
 515 520 525
 Ser Gly Ile Pro Ala Asn Gln His Arg Leu Thr Leu Thr Arg Leu
 530 535 540
 Asp Pro Gly Ser Leu Tyr Glu Val Glu Met Ala Ala Tyr Asn Cys
 545 550 555
 Ala Gly Glu Gly Gln Thr Ala Met Val Thr Phe Arg Thr Gly Arg

560	565	570
Arg Pro Lys Pro Glu Ile Met Ala Ser Lys	Glu Gln Gln Ile Gln	
575	580	585
Arg Asp Asp Pro Gly Ala Ser Pro Gln Ser Ser Ser Gln Pro Asp		
590	595	600
His Gly Arg Leu Ser Pro Pro Glu Ala Pro Asp Arg Pro Thr Ile		
605	610	615
Ser Thr Ala Ser Glu Thr Ser Val Tyr Val Thr Trp Ile Pro Arg		
620	625	630
Gly Asn Gly Gly Phe Pro Ile Gln Ser Phe Arg Val Glu Tyr Lys		
635	640	645
Lys Leu Lys Lys Val Gly Asp Trp Ile Leu Ala Thr Ser Ala Ile		
650	655	660
Pro Pro Ser Arg Leu Ser Val Glu Ile Thr Gly Leu Glu Lys Gly		
665	670	675
Thr Ser Tyr Lys Phe Arg Val Arg Ala Leu Asn Met Leu Gly Glu		
680	685	690
Ser Glu Pro Ser Ala Pro Ser Arg Pro Tyr Val Val Ser Gly Tyr		
695	700	705
Ser Gly Arg Val Tyr Glu Arg Pro Val Ala Gly Pro Tyr Ile Thr		
710	715	720
Phe Thr Asp Ala Val Asn Glu Thr Thr Ile Met Leu Lys Trp Met		
725	730	735
Tyr Ile Pro Ala Ser Asn Asn Asn Thr Pro Ile His Gly Phe Tyr		
740	745	750
Ile Tyr Tyr Arg Pro Thr Asp Ser Asp Asn Asp Ser Asp Tyr Lys		
755	760	765
Lys Asp Met Val Glu Gly Asp Lys Tyr Trp His Ser Ile Ser His		
770	775	780
Leu Gln Pro Glu Thr Ser Tyr Asp Ile Lys Met Gln Cys Phe Asn		
785	790	795
Glu Gly Gly Glu Ser Glu Phe Ser Asn Val Met Ile Cys Glu Thr		
800	805	810
Lys Ala Arg Lys Ser Ser Gly Gln Pro Gly Arg Leu Pro Pro Pro		
815	820	825
Thr Leu Ala Pro Pro Gln Pro Pro Leu Pro Glu Thr Ile Glu Arg		
830	835	840
Pro Val Gly Thr Gly Ala Met Val Ala Arg Ser Ser Asp Leu Pro		
845	850	855

Tyr Leu Ile Val Gly Val Val Leu Gly Ser Ile Val Leu Ile Ile
 860 865 870
 Val Thr Phe Ile Pro Phe Cys Leu Trp Arg Ala Trp Ser Lys Gln
 875 880 885
 Lys His Thr Thr Asp Leu Gly Phe Pro Arg Ser Ala Leu Pro Pro
 890 895 900
 Ser Cys Pro Tyr Thr Met Val Pro Leu Gly Gly Leu Pro Gly His
 905 910 915
 Gln Ala Ser Gly Gln Pro Tyr Leu Ser Gly Ile Ser Gly Arg Ala
 920 925 930
 Cys Ala Asn Gly Ile His Met Asn Arg Gly Cys Pro Ser Ala Ala
 935 940 945
 Val Gly Tyr Pro Gly Met Lys Pro Gln Gln His Cys Pro Gly Glu
 950 955 960
 Leu Gln Gln Gln Ser Asp Thr Ser Ser Leu Leu Arg Gln Thr His
 965 970 975
 Leu Gly Asn Gly Tyr Asp Pro Gln Ser His Gln Ile Thr Arg Gly
 980 985 990
 Pro Lys Ser Ser Pro Asp Glu Gly Ser Phe Leu Tyr Thr Leu Pro
 995 1000 1005
 Asp Asp Ser Thr His Gln Leu Leu Gln Pro His His Asp Cys Cys
 1010 1015 1020
 Gln Arg Gln Glu Gln Pro Ala Ala Val Gly Gln Ser Gly Val Arg
 1025 1030 1035
 Arg Ala Pro Asp Ser Pro Val Leu Glu Ala Val Trp Asp Pro Pro
 1040 1045 1050
 Phe His Ser Gly Pro Pro Cys Cys Leu Gly Leu Val Pro Val Glu
 1055 1060 1065
 Glu Val Asp Ser Pro Asp Ser Cys Gln Val Ser Gly Gly Asp Trp
 1070 1075 1080
 Cys Pro Gln His Pro Val Gly Ala Tyr Val Gly Gln Glu Pro Gly
 1085 1090 1095
 Met Gln Leu Ser Pro Gly Pro Leu Val Arg Val Ser Phe Glu Thr
 1100 1105 1110
 Pro Pro Leu Thr Ile
 1115

<210> 59
 <211> 25
 <212> DNA
 <213> Artificial

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<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 59
      gggaaacaca gcagtcattg cctgc 25

<210> 60
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-24
<223> Synthetic construct.

<400> 60
      gcacacgttag cctgtcgctg gagc 24

<210> 61
<211> 42
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-42
<223> Synthetic construct.

<400> 61
      caccccaaag cccaggtccg gtacagcgtc aaacaagagt gg 42

<210> 62
<211> 1661
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 678
<223> unknown base

<400> 62
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      cgcctgctcc tcccaggctc ccgcggccga cccccgcgca acatgcagcc 100
      cacgggccgc gagggttccc gcgcgctcag ccggcggtat ctgcggcg 150
      tgctgctcct gctactgctg ctgctgctgc ggcagccgt aaccgcgcg 200
      gagaccacgc cggcgcccc cagagccctc tccacgctgg gtcggcc 250
      cctcttacc accgggggtg tccccagcgc cctcaactacc ccaggccta 300
      ctacgccagg caccccaaa accctggacc ttctgggtcg cgccgaggcc 350

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ctgatgcgga gtttcccact cgtggacggc cacaatgacc tgccccaggt 400
cctgagacag cgttacaaga atgtgcttca ggtatgttaac ctgcgaaatt 450
tcagccatgg tcagaccaggc ctggacaggc ttagagacgg cctcggtgg 500
gcccagttct ggtcagcctc cgtctcatgc cagtcccagg accagactgc 550
cgtgcgcctc gccctggagc agattgacct cattcaccgc atgtgtgcct 600
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caaaagctgg cctgcctcat tggcgtgnag ggtggtaact cactggacag 700
cagcctctct gtgctgcgca gtttctatgt gctgggggtg cgctacctga 750
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tcccgtatgt atcctgcagc ttctgaagaa cgggtggcatc gtgatggta 1050
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gccccctctc ctagttcatt cacaagcata tgctgagaat aaacatgtta 1650
cacatggaaa a 1661

<210> 63
<211> 487
<212> PRT
<213> Homo sapiens

<220>
 <221> unsure
 <222> 196, 386
 <223> unknown amino acid

<400> 63

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Tyr Leu Arg Arg Leu Leu Leu Leu Leu Leu Leu Leu Leu Arg
 20 25 30

Gln Pro Val Thr Arg Ala Glu Thr Thr Pro Gly Ala Pro Arg Ala
 35 40 45

Leu Ser Thr Leu Gly Ser Pro Ser Leu Phe Thr Thr Pro Gly Val
 50 55 60

Pro Ser Ala Leu Thr Thr Pro Gly Leu Thr Thr Pro Gly Thr Pro
 65 70 75

Lys Thr Leu Asp Leu Arg Gly Arg Ala Gln Ala Leu Met Arg Ser
 80 85 90

Phe Pro Leu Val Asp Gly His Asn Asp Leu Pro Gln Val Leu Arg
 95 100 105

Gln Arg Tyr Lys Asn Val Leu Gln Asp Val Asn Leu Arg Asn Phe
 110 115 120

Ser His Gly Gln Thr Ser Leu Asp Arg Leu Arg Asp Gly Leu Val
 125 130 135

Gly Ala Gln Phe Trp Ser Ala Ser Val Ser Cys Gln Ser Gln Asp
 140 145 150

Gln Thr Ala Val Arg Leu Ala Leu Glu Gln Ile Asp Leu Ile His
 155 160 165

Arg Met Cys Ala Ser Tyr Ser Glu Leu Glu Leu Val Thr Ser Ala
 170 175 180

Glu Gly Leu Asn Ser Ser Gln Lys Leu Ala Cys Leu Ile Gly Val
 185 190 195

Xaa Gly Gly His Ser Leu Asp Ser Ser Leu Ser Val Leu Arg Ser
 200 205 210

Phe Tyr Val Leu Gly Val Arg Tyr Leu Thr Leu Thr Phe Thr Cys
 215 220 225

Ser Thr Pro Trp Ala Glu Ser Ser Thr Lys Phe Arg His His Met
 230 235 240

Tyr Thr Asn Val Ser Gly Leu Thr Ser Phe Gly Glu Lys Val Val
 245 250 255

Glu Glu Leu Asn Arg Leu Gly Met Met Ile Asp Leu Ser Tyr Ala

260	265	270
Ser Asp Thr Leu Ile Arg Arg Val Leu Glu Val Ser Gln Ala Pro		
275	280	285
Val Ile Phe Ser His Ser Ala Ala Arg Ala Val Cys Asp Asn Leu		
290	295	300
Leu Asn Val Pro Asp Asp Ile Leu Gln Leu Leu Lys Asn Gly Gly		
305	310	315
Ile Val Met Val Thr Leu Ser Met Gly Val Leu Gln Cys Asn Leu		
320	325	330
Leu Ala Asn Val Ser Thr Val Ala Asp His Phe Asp His Ile Arg		
335	340	345
Ala Val Ile Gly Ser Glu Phe Ile Gly Ile Gly Gly Asn Tyr Asp		
350	355	360
Gly Thr Gly Arg Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr		
365	370	375
Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Xaa Trp Ser Glu Glu		
380	385	390
Glu Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg		
395	400	405
Gln Val Glu Lys Val Arg Glu Glu Ser Arg Ala Gln Ser Pro Val		
410	415	420
Glu Ala Glu Phe Pro Tyr Gly Gln Leu Ser Thr Ser Cys His Ser		
425	430	435
His Leu Val Pro Gln Asn Gly His Gln Ala Thr His Leu Glu Val		
440	445	450
Thr Lys Gln Pro Thr Asn Arg Val Pro Trp Arg Ser Ser Asn Ala		
455	460	465
Ser Pro Tyr Leu Val Pro Gly Leu Val Ala Ala Ala Thr Ile Pro		
470	475	480
Thr Phe Thr Gln Trp Leu Cys		
485		

<210> 64
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 64

ccttcacctg cagtacacca tggc 25
<210> 65
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 65
gtcacacaca gctctggcag ctgag 25

<210> 66
<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-47
<223> Synthetic construct.

<400> 66
ccaagttcag acaccacatg tacaccaacg tcagcggatt gacaagc 47

<210> 67
<211> 1564
<212> DNA
<213> Homo sapiens

<400> 67
tgctaggctc tgtcccacaa tgcacccgag agcaggagct gaaagcctct 50
aacacccaca gatccctcta tgactgcaat gtgaggtgtc cggctttgct 100
ggcccagcaa gcctgataag catgaagctc ttatcttgg tggctgttgt 150
cgggtgtttg ctggtgcccc cagctgaagc caacaagagt tctgaagata 200
tccggtgcaa atgcatctgt ccaccttata gaaacatcag tggcacatt 250
tacaaccaga atgtatccca gaaggactgc aactgcctgc acgtggtgaa 300
gcccatgcca gtgcctggcc atgacgtgaa ggcctactgc ctgctgtgcg 350
agtgcaggta cgaggagcgc agcaccacca ccatcaaggt catcattgtc 400
atctacctgt ccgtggtgaa tgccctgttg ctctacatgg ccttcctgat 450
gctggtgac cctctgatcc gaaagccgga tgcatacact gagcaactgc 500
acaatgagga ggagaatgag gatgctcgct ctatggcagc agctgctgca 550
tccctcgaaa gaccccgagc aaacacagtc ctggagcgtg tggaaagggtgc 600

ccagcagcgg tggaagctgc aggtgcagga gcagcggaaag acagtcttcg 650
 atcggcacaa gatgctcagc tagatgggct ggtgtggttg ggtcaaggcc 700
 ccaacaccat ggctgccagc ttccaggctg gacaaagcag ggggctactt 750
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 aagagggatg tggctctga tctctgttgt cttctgggt ctgggggtt 900
 gaagggaggg ggaaggcagg ccagaaggaa atggagacat tcgaggcggc 950
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 gcctcttgc cctgaacttc gttgtaccag tgcatggaga gaaaattttg 1500
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 ttttatttct ctca 1564

<210> 68
 <211> 183
 <212> PRT
 <213> Homo sapiens

<400> 68
 Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val
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 Pro Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys
 20 25 30
 Cys Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn
 35 40 45
 Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu
 50 55 60

Pro	Met	Pro	Val	Pro	Gly	His	Asp	Val	Glu	Ala	Tyr	Cys	Leu	Leu
				65					70					75
Cys	Glu	Cys	Arg	Tyr	Glu	Glu	Arg	Ser	Thr	Thr	Thr	Ile	Lys	Val
				80					85					90
Ile	Ile	Val	Ile	Tyr	Leu	Ser	Val	Val	Gly	Ala	Leu	Leu	Leu	Tyr
				95					100					105
Met	Ala	Phe	Leu	Met	Leu	Val	Asp	Pro	Leu	Ile	Arg	Lys	Pro	Asp
				110					115					120
Ala	Tyr	Thr	Glu	Gln	Leu	His	Asn	Glu	Glu	Glu	Asn	Glu	Asp	Ala
				125					130					135
Arg	Ser	Met	Ala	Ala	Ala	Ala	Ser	Leu	Gly	Gly	Pro	Arg	Ala	
				140					145					150
Asn	Thr	Val	Leu	Glu	Arg	Val	Glu	Gly	Ala	Gln	Gln	Arg	Trp	Lys
				155					160					165
Leu	Gln	Val	Gln	Glu	Gln	Arg	Lys	Thr	Val	Phe	Asp	Arg	His	Lys
				170					175					180
Met	Leu	Ser												

<210> 69
<211> 3170
<212> DNA
<213> Homo sapiens

<400> 69
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tccctttgca ttccccacccc tccgggcttt gcgttctcct ggggacccccc 200
tcgcccggag atggccgcgt tgatgcggag caaggattcg tcctgctgcc 250
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gtccaccctt ttaaaaatta ttatttgaag taatttattt acaggaaatg 3000
ttaatgagat gtatttctt atagagatat ttcttacaga aagctttgt 3050
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taagataaaaa tctattaaat tttcttcctc taaaaactga aaaaaaaaaa 3150
aaaaaaaaaaaa aaaaaaaaaa 3170

<210> 70
<211> 259
<212> PRT
<213> Homo sapiens

<400> 70
Met Ala Ala Leu Met Arg Ser Lys Asp Ser Ser Cys Cys Leu Leu
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Leu Leu Ala Ala Val Leu Met Val Glu Ser Ser Gln Ile Gly Ser
20 25 30
Ser Arg Ala Lys Leu Asn Ser Ile Lys Ser Ser Leu Gly Gly Glu
35 40 45

Thr Pro Gly Gln Ala Ala Asn Arg Ser Ala Gly Met Tyr Gln Gly
 50 55 60
 Leu Ala Phe Gly Gly Ser Lys Lys Gly Lys Asn Leu Gly Gln Ala
 65 70 75
 Tyr Pro Cys Ser Ser Asp Lys Glu Cys Glu Val Gly Arg Tyr Cys
 80 85 90
 His Ser Pro His Gln Gly Ser Ser Ala Cys Met Val Cys Arg Arg
 95 100 105
 Lys Lys Lys Arg Cys His Arg Asp Gly Met Cys Cys Pro Ser Thr
 110 115 120
 Arg Cys Asn Asn Gly Ile Cys Ile Pro Val Thr Glu Ser Ile Leu
 125 130 135
 Thr Pro His Ile Pro Ala Leu Asp Gly Thr Arg His Arg Asp Arg
 140 145 150
 Asn His Gly His Tyr Ser Asn His Asp Leu Gly Trp Gln Asn Leu
 155 160 165
 Gly Arg Pro His Thr Lys Met Ser His Ile Lys Gly His Glu Gly
 170 175 180
 Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly Phe Cys Cys
 185 190 195
 Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu His Gln
 200 205 210
 Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly Leu
 215 220 225
 Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys
 230 235 240
 Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val
 245 250 255
 Cys Gln Lys Ile

<210> 71
 <211> 1809
 <212> DNA
 <213> Homo sapiens

<400> 71
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 tggcctccca aagtgttggg attacaggcg tgagccaccg cgccccggcca 100
 acatcacgtt tttaaaaatt gatttcttca aattcatggc aaatatttcc 150
 cttcccttta acttcttata tcagaatgag gaaggatagc tgcatttt 200

tagtcagtt tcattgcata gtaatatttt catgtatcat tttctaagtt 250
atattttagt aattcatatg ttttagatta taggtttaa catacttgt 300
aaaatactg atgtgttta aagccttggg cagaaattct gtattgttga 350
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gtacacagca gaatagtaca agtcacccta caactactac ttcttgggac 550
ctcaagcccc caacatccca gtcctcagtc ctcagtcate ttgacttcaa 600
atctcaacct gagccatccc cagttcttag ccagttgagc cagcgacaaac 650
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ccttcccagg caaaaacttcg agaatcaaca cctggagaca gtccctccac 750
tgtgaacaag ctttgcagc ttcccagcac gaccattgaa aatatctctg 800
tgtctgtcca ccagccacag cccaaacaca tcaaacttgc taagcggcgg 850
ataccccccag cttctaagat cccagttct gcagtgaaa tgccctgggtc 900
agcagatgtc acaggattaa atgtgcagtt tgggctctg gaatttgggt 950
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aatcagattc ccatcagtt gtattcgaag tcttaagtgc agcctttgaa 1050
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ccgtcattac ctcctgcagt ctgacaagct catcaactgaa ttctgtctgt 1150
ccagtagcaa tgtcttcctc ttatgaccag agttctgtgc ataacaggat 1200
cccataccaa agccctgtga gttcatcaga gtcagctcca ggaaccatca 1250
tgaatggaca tgggtgggt cgaagtcagc agacactaga cagtaagtat 1300
agcagcaagc tactttgtc atggctgggt ccaacccaaac agaggaagag 1350
gatagctcac gtgatgtgga aaacaccagt tggtaatgg ctcattcgtt 1400
aaaaagcagc cctttgcctt tttgtttt ggaccaggtg ttggctgtgg 1450
tgttattaga aatgtcttaa ccacagcaag aaggagggtgg tggtctcata 1500
ttcttctgcc ctaatcagac tgcaccacaa gtgcagcata cagttatgt 1550
tttaaagatg cttggccag gcgggggtggc tggatgccc aatcccagtg 1600
cttgggggg ccaaggcagg cagattgccc aagctcagga gtttgagacc 1650

accctggca acatggtaa actctgtctc tactaaaata cgaaaaacta 1700
gccgggtgtg gtggccgcgc gtgcctgtaa tcccagctac ttgggaggct 1750
gaggcacaag aatcgcttga gccagcttgg gctacaaagt gagactccgt 1800
ctgaaaaga 1809

<210> 72
<211> 363
<212> PRT
<213> Homo sapiens

<400> 72
Met Cys Phe Lys Ala Leu Gly Arg Asn Ser Val Leu Leu Arg Ile
1 5 10 15
Cys Ser Phe Ile Pro Leu Leu Lys Ser Ser Val Leu Gly Ser Gly
20 25 30
Phe Gly Glu Leu Ala Pro Pro Lys Met Ala Asn Ile Thr Ser Ser
35 40 45
Gln Ile Leu Asp Gln Leu Lys Ala Pro Ser Leu Gly Gln Phe Thr
50 55 60
Thr Thr Pro Ser Thr Gln Gln Asn Ser Thr Ser His Pro Thr Thr
65 70 75
Thr Thr Ser Trp Asp Leu Lys Pro Pro Thr Ser Gln Ser Ser Val
80 85 90
Leu Ser His Leu Asp Phe Lys Ser Gln Pro Glu Pro Ser Pro Val
95 100 105
Leu Ser Gln Leu Ser Gln Arg Gln Gln His Gln Ser Gln Ala Val
110 115 120
Thr Val Pro Pro Pro Gly Leu Glu Ser Phe Pro Ser Gln Ala Lys
125 130 135
Leu Arg Glu Ser Thr Pro Gly Asp Ser Pro Ser Thr Val Asn Lys
140 145 150
Leu Leu Gln Leu Pro Ser Thr Thr Ile Glu Asn Ile Ser Val Ser
155 160 165
Val His Gln Pro Gln Pro Lys His Ile Lys Leu Ala Lys Arg Arg
170 175 180
Ile Pro Pro Ala Ser Lys Ile Pro Ala Ser Ala Val Glu Met Pro
185 190 195
Gly Ser Ala Asp Val Thr Gly Leu Asn Val Gln Phe Gly Ala Leu
200 205 210
Glu Phe Gly Ser Glu Pro Ser Leu Ser Glu Phe Gly Ser Ala Pro
215 220 225

Ser Ser Glu Asn Ser Asn Gln Ile Pro Ile Ser Leu Tyr Ser Lys
 230 235 240
 Ser Leu Ser Glu Pro Leu Asn Thr Ser Leu Ser Met Thr Ser Ala
 245 250 255
 Val Gln Asn Ser Thr Tyr Thr Ser Val Ile Thr Ser Cys Ser
 260 265 270
 Leu Thr Ser Ser Ser Leu Asn Ser Ala Ser Pro Val Ala Met Ser
 275 280 285
 Ser Ser Tyr Asp Gln Ser Ser Val His Asn Arg Ile Pro Tyr Gln
 290 295 300
 Ser Pro Val Ser Ser Ser Glu Ser Ala Pro Gly Thr Ile Met Asn
 305 310 315
 Gly His Gly Gly Arg Ser Gln Gln Thr Leu Asp Ser Lys Tyr
 320 325 330
 Ser Ser Lys Leu Leu Leu Ser Trp Leu Val Pro Thr Lys Gln Arg
 335 340 345
 Lys Arg Ile Ala His Val Met Trp Lys Thr Pro Val Gly Gln Trp
 350 355 360
 Leu Ile Arg

<210> 73
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 73
 aattcatggc aaatatttcc cttccc 26

<210> 74
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 74
 tggtaaactg gcccaaactc gg 22

<210> 75
 <211> 50

<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-50
<223> Synthetic construct

<400> 75
ttaaagtcat ccgtccttgg ctcaggattt ggagagcttg caccaccaaa 50

<210> 76
<211> 1989
<212> DNA
<213> Homo sapiens

<400> 76
gccgagtgccc acaaaggcctg gggctggcg gggccatgg cgctgccatc 50
ccgaatcctg ctttgaaac ttgtgcttct gcagagctct gctgttctcc 100
tgcaactcagc ggtggaggag acggacgcgg ggctgtacac ctgcaacctg 150
caccatcact actgccaccc ttagagacgc ctggccgtcc gcctggaggt 200
caccgacggc ccccccggcca ccccccgccta ctggacggc gagaaggagg 250
tgctggcggt ggcgcgcggc gcacccgcgc ttctgacctg cgtgaaccgc 300
gggcacgtgt ggaccgaccg gcacgtggag gaggctaac aggtggtgca 350
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cgcgaccgcg tggctgtgg cgccgatgcc tttgagcgcg gtgacttctc 500
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gccacaacgt catcaatgtc atcgccccg agagccgagc ccacttcttc 750
cagcagctgg gctacgtgct ggccacgcgt ctgctttca tcctgctact 800
ggtcactgtc ctccctggccc cccgcaggcg ccgcggaggc tacgaatact 850
cgaccagaag gtcggaaag tcaaaggaaa aggatgttaa ctggcggag 900
ttcgctgtgg ctgcaggaaa ccagatgctt tacaggagtg aggacatcca 950
gcttagattac aaaaacaaca tcctgaagga gagggcggag ctggcccaca 1000
ccccccctgcc tgccaagtac atcgacctag acaaagggtt ccggaaggag 1050

aactgcaaat agggaggccc tgggctcctg gctgggccag cagctgcacc 1100
tctcctgtct gtgctcctcg gggcatctcc tcatgtccg gggctcaccc 1150
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agaggccgcc tccacacccc tcccccaaggc gcttggtggc agcatagccc 1250
ccacccctgc ggccttgct cacgggtggc cctgcccacc cctggcaca 1300
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cagccccaaa actggggta gcctcaggc aggagtccca ctccctccagg 1450
gctctgctcg tccggggctg ggagatgttc ctggaggagg acactccat 1500
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ctgcccatttc tctgccccat ccctacccta gccttgctct cagccaccc 1750
gatagtcact gggctccctg tgacttctga ccctgacacc cctcccttgg 1800
actctgcctg ggctggagtc tagggctggg gctacatttgc ttctgtac 1850
tggctgagga caggggaggg agtgaagttg gttgggggtg gcctgtgtt 1900
ccactctcag cacccacat ttgcatttc tggtggaccc gccaccatca 1950
caataaagtc cccatctgat ttttaaaaaa aaaaaaaaaa 1989

<210> 77
<211> 341
<212> PRT
<213> Homo sapiens

<400> 77
Met Ala Leu Pro Ser Arg Ile Leu Leu Trp Lys Leu Val Leu Leu
1 5 10 15
Gln Ser Ser Ala Val Leu Leu His Ser Ala Val Glu Glu Thr Asp
20 25 30
Ala Gly Leu Tyr Thr Cys Asn Leu His His His Tyr Cys His Leu
35 40 45
Tyr Glu Ser Leu Ala Val Arg Leu Glu Val Thr Asp Gly Pro Pro
50 55 60
Ala Thr Pro Ala Tyr Trp Asp Gly Glu Lys Glu Val Leu Ala Val
65 70 75

Ala Arg Gly Ala Pro Ala Leu Leu Thr Cys Val Asn Arg Gly His
 80 85 90
 Val Trp Thr Asp Arg His Val Glu Glu Ala Gln Gln Val Val His
 95 100 105
 Trp Asp Arg Gln Pro Pro Gly Val Pro His Asp Arg Ala Asp Arg
 110 115 120
 Leu Leu Asp Leu Tyr Ala Ser Gly Glu Arg Arg Ala Tyr Gly Pro
 125 130 135
 Leu Phe Leu Arg Asp Arg Val Ala Val Gly Ala Asp Ala Phe Glu
 140 145 150
 Arg Gly Asp Phe Ser Leu Arg Ile Glu Pro Leu Glu Val Ala Asp
 155 160 165
 Glu Gly Thr Tyr Ser Cys His Leu His His Tyr Cys Gly Leu
 170 175 180
 His Glu Arg Arg Val Phe His Leu Thr Val Ala Glu Pro His Ala
 185 190 195
 Glu Pro Pro Pro Arg Gly Ser Pro Gly Asn Gly Ser Ser His Ser
 200 205 210
 Gly Ala Pro Gly Pro Asp Pro Thr Leu Ala Arg Gly His Asn Val
 215 220 225
 Ile Asn Val Ile Val Pro Glu Ser Arg Ala His Phe Phe Gln Gln
 230 235 240
 Leu Gly Tyr Val Leu Ala Thr Leu Leu Leu Phe Ile Leu Leu Leu
 245 250 255
 Val Thr Val Leu Leu Ala Ala Arg Arg Arg Gly Gly Tyr Glu
 260 265 270
 Tyr Ser Asp Gln Lys Ser Gly Lys Ser Lys Gly Lys Asp Val Asn
 275 280 285
 Leu Ala Glu Phe Ala Val Ala Ala Gly Asp Gln Met Leu Tyr Arg
 290 295 300
 Ser Glu Asp Ile Gln Leu Asp Tyr Lys Asn Asn Ile Leu Lys Glu
 305 310 315
 Arg Ala Glu Leu Ala His Ser Pro Leu Pro Ala Lys Tyr Ile Asp
 320 325 330
 Leu Asp Lys Gly Phe Arg Lys Glu Asn Cys Lys
 335 340

<210> 78
 <211> 2243
 <212> DNA
 <213> Homo sapiens

<400> 78
cgccggaggc agccggcg tggcgacgcg ggcacatggc cgttgtctca 50
gaggacgact ttcaagcacag ttcaaactcc acctacggaa ccacaagcag 100
cagtctccga gctgaccagg aggcaactgt tgagaagctg ctggaccgcc 150
cgccccctgg cctgcagagg cccgaggacc gcttctgtgg cacatacatc 200
atcttcttca gcctggcat tggcagtcta ctgccatgga acttctttat 250
caactgccaag gagtaactgga tggtaactact ccgcaactcc tccagcccag 300
ccaccgggga ggaccctgag ggctcagaca tcctgaacta ctggagagc 350
taccttgccg ttgcctccac cgtgcctcc atgctgtgcc tggtgccaa 400
cttcctgctt gtcaacaggg ttgcagtcca catccgtgc ctggcctcac 450
tgacggcat cctggccatc ttcatggtga taactgcact ggtgaaggtg 500
gacacttcct cctggaccgg tggttttttt gcggcacca ttgtctgcat 550
ggtgatcctc agcgggcct ccactgtctt cagcagcagc atctacggca 600
tgaccggctc ctttcctatg aggaactccc aagcaactgat atcaggagga 650
gccatggcg ggacggtcag cggcggtgg tcattggtgg acttggctgc 700
atccagtgat gtgaggaaca gcgcctggc ctttttcctg acggccacca 750
tcttcctcgat gctctgcatg ggactctacc tgctgtgtc caggctggag 800
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agattgtgcc caggagctg gctgaggcca cgggagtggt gatgtccctt 1400
tatgtgtgct tggcttaac actgggctca gcctgctcta ccctcctggt 1450

gcacccatc tagaaggag gacacaagga cattggctc tcagagcctt 1500
tgaagatgag aagagagtgc aggagggctg gggccatgg agggaaaggcc 1550
taaagttca cttgggaca gagagcagag cacactcggt cctcatccct 1600
cccaagatgc cagtggcca cgtccatgcc cattccgtgc aaggcagata 1650
ttccagtcattaaacagaa cactcctgag acagttgaag aagaaatagc 1700
acaaatcagg ggtactccct tcacagctga tggtaacat tccacccttct 1750
ttcttagccct tcaaagatgc tgccagtg ttcccttagag ttattacaaa 1800
gccagtgcca aaacccagcc atgggcttgc tgcaacctcc cagctgcgt 1850
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ccaagactca agtgtgcaca gaccctgtt ttctgcgggtt gaacaactgc 2000
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cctgggtcaa gatgagggtc tttcagtg ttctgttaca acatgtcaaa 2200
gccattggttt caagggcgta ataaatactt gcgtattcaa aaa 2243

<210> 79

<211> 475

<212> PRT

<213> Homo sapiens

<400> 79

Met	Ala	Val	Val	Ser	Glu	Asp	Asp	Phe	Gln	His	Ser	Ser	Asn	Ser
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Thr	Tyr	Gly	Thr	Thr	Ser	Ser	Ser	Leu	Arg	Ala	Asp	Gln	Glu	Ala
								20		25			30	
Leu	Leu	Glu	Lys	Leu	Leu	Asp	Arg	Pro	Pro	Pro	Gly	Leu	Gln	Arg
						35			40			45		
Pro	Glu	Asp	Arg	Phe	Cys	Gly	Thr	Tyr	Ile	Ile	Phe	Phe	Ser	Leu
				50					55			60		
Gly	Ile	Gly	Ser	Leu	Leu	Pro	Trp	Asn	Phe	Phe	Ile	Thr	Ala	Lys
						65			70			75		
Glu	Tyr	Trp	Met	Phe	Lys	Leu	Arg	Asn	Ser	Ser	Ser	Pro	Ala	Thr
				80				85				90		
Gly	Glu	Asp	Pro	Glu	Gly	Ser	Asp	Ile	Leu	Asn	Tyr	Phe	Glu	Ser
					95				100			105		

Tyr Leu Ala Val Ala Ser Thr Val Pro Ser Met Leu Cys Leu Val
 110 115 120
 Ala Asn Phe Leu Leu Val Asn Arg Val Ala Val His Ile Arg Val
 125 130 135
 Leu Ala Ser Leu Thr Val Ile Leu Ala Ile Phe Met Val Ile Thr
 140 145 150
 Ala Leu Val Lys Val Asp Thr Ser Ser Trp Thr Arg Gly Phe Phe
 155 160 165
 Ala Val Thr Ile Val Cys Met Val Ile Leu Ser Gly Ala Ser Thr
 170 175 180
 Val Phe Ser Ser Ser Ile Tyr Gly Met Thr Gly Ser Phe Pro Met
 185 190 195
 Arg Asn Ser Gln Ala Leu Ile Ser Gly Gly Ala Met Gly Gly Thr
 200 205 210
 Val Ser Ala Val Ala Ser Leu Val Asp Leu Ala Ala Ser Ser Asp
 215 220 225
 Val Arg Asn Ser Ala Leu Ala Phe Phe Leu Thr Ala Thr Ile Phe
 230 235 240
 Leu Val Leu Cys Met Gly Leu Tyr Leu Leu Ser Arg Leu Glu
 245 250 255
 Tyr Ala Arg Tyr Tyr Met Arg Pro Val Leu Ala Ala His Val Phe
 260 265 270
 Ser Gly Glu Glu Glu Leu Pro Gln Asp Ser Leu Ser Ala Pro Ser
 275 280 285
 Val Ala Ser Arg Phe Ile Asp Ser His Thr Pro Pro Leu Arg Pro
 290 295 300
 Ile Leu Lys Lys Thr Ala Ser Leu Gly Phe Cys Val Thr Tyr Val
 305 310 315
 Phe Phe Ile Thr Ser Leu Ile Tyr Pro Ala Val Cys Thr Asn Ile
 320 325 330
 Glu Ser Leu Asn Lys Gly Ser Gly Ser Leu Trp Thr Thr Lys Phe
 335 340 345
 Phe Ile Pro Leu Thr Thr Phe Leu Leu Tyr Asn Phe Ala Asp Leu
 350 355 360
 Cys Gly Arg Gln Leu Thr Ala Trp Ile Gln Val Pro Gly Pro Asn
 365 370 375
 Ser Lys Ala Leu Pro Gly Phe Val Leu Leu Arg Thr Cys Leu Ile
 380 385 390
 Pro Leu Phe Val Leu Cys Asn Tyr Gln Pro Arg Val His Leu Lys

395	400	405
Thr Val Val Phe Gln Ser Asp Val Tyr Pro Ala Leu Leu Ser Ser		
410	415	420
Leu Leu Gly Leu Ser Asn Gly Tyr Leu Ser Thr Leu Ala Leu Leu		
425	430	435
Tyr Gly Pro Lys Ile Val Pro Arg Glu Leu Ala Glu Ala Thr Gly		
440	445	450
Val Val Met Ser Phe Tyr Val Cys Leu Gly Leu Thr Leu Gly Ser		
455	460	465
Ala Cys Ser Thr Leu Leu Val His Leu Ile		
470	475	

<210> 80
<211> 22
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-22
<223> Synthetic construct.

<400> 80
tttgcggtc accattgtct gc 22

<210> 81
<211> 23
<212> DNA
<213> Homo sapiens

<220>
<221> Artificial sequence
<222> 1-23
<223> Synthetic construct.

<400> 81
cgttaggtgac acagaagccc agg 23

<210> 82
<211> 49
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-49
<223> Synthetic construct.

<400> 82
tacggcatga ccggctcctt tcctatgagg aactccagg cactgatat 49

<210> 83
<211> 1844

<212> DNA
<213> Homo sapiens

<400> 83
gacagtggag ggcagtggag aggaccgcgc tgtcctgctg tcaccaagag 50
ctggagacac catctccac cgagagtcat ggccccattt gccctgcacc 100
tcctcgctt cgtccccatc ctcctcagcc tgggtggcctc ccaggactgg 150
aaggctgaac gcagccaaga ccccttcgag aaatgcattc aggtatcctga 200
ctatgagcag ctgctcaagg tggtgacactg ggggctcaat cggaccctga 250
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gccaagggtgc tcagcgatgc tggacacaag gtcaccatcc tggaggcaga 350
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ggattgggaa gctggggagcc atgcgcattc ccagctctca caggatcctc 450
cacaagctct gccaggccc ggggctcaac ctgaccaagt tcacccagta 500
cgacaagaac acgtggacgg aggtgcacga agtgaagctg cgcaactatg 550
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aagggccact cgcccgaaaga catctaccatc atggctctca accaggccct 650
caaagacctc aaggcactgg gctgcagaaa ggcgatgaag aagtttgaaa 700
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gcccgtgcagc ttctggaga cgttatgtcc gaggatggct tcttctatct 800
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ccagggaccgg cacgatgtgc acgtgcagat cgagacctct ccccccggcgc 1000
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ccggcttggat ccgggaagag gcgttgcgt tggcgctcga cgacgtggcg 1350

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gacggcggtc aagtccggcgc tgccgcgc catcaagatc aacagccgga 1600
aggggcctgc atccggacacg gccagccccg aggggcacgc atctgacatg 1650
gaggggcagg ggcatgtgca tgggtggcc agcagccct cgcacatg 1700
ggcaaaggaa gaaggcagcc accctccagt ccaaggccag ttatctctcc 1750
aaaacacgac ccacacgagg acctcgcat aaagtattt cgaaaaaaa 1800
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1844

<210> 84

<211> 567

<212> PRT

<213> Homo sapiens

<400> 84

Met	Ala	Pro	Leu	Ala	Leu	His	Leu	Leu	Val	Leu	Val	Pro	Ile	Leu
1														15
Leu	Ser	Leu	Val	Ala	Ser	Gln	Asp	Trp	Lys	Ala	Glu	Arg	Ser	Gln
														30
Asp	Pro	Phe	Glu	Lys	Cys	Met	Gln	Asp	Pro	Asp	Tyr	Glu	Gln	Leu
														45
Leu	Lys	Val	Val	Thr	Trp	Gly	Leu	Asn	Arg	Thr	Leu	Lys	Pro	Gln
														60
Arg	Val	Ile	Val	Val	Gly	Ala	Gly	Val	Ala	Gly	Leu	Val	Ala	Ala
														75
Lys	Val	Leu	Ser	Asp	Ala	Gly	His	Lys	Val	Thr	Ile	Leu	Glu	Ala
														90
Asp	Asn	Arg	Ile	Gly	Gly	Arg	Ile	Phe	Thr	Tyr	Arg	Asp	Gln	Asn
														105
Thr	Gly	Trp	Ile	Gly	Glu	Leu	Gly	Ala	Met	Arg	Met	Pro	Ser	Ser
														120
His	Arg	Ile	Leu	His	Lys	Leu	Cys	Gln	Gly	Leu	Gly	Leu	Asn	Leu
														135
Thr	Lys	Phe	Thr	Gln	Tyr	Asp	Lys	Asn	Thr	Trp	Thr	Glu	Val	His
														150
Glu	Val	Lys	Leu	Arg	Asn	Tyr	Val	Val	Glu	Lys	Val	Pro	Glu	Lys
														165
155														

Leu Gly Tyr Ala Leu Arg Pro Gln Glu Lys Gly His Ser Pro Glu
 170 175 180
 Asp Ile Tyr Gln Met Ala Leu Asn Gln Ala Leu Lys Asp Leu Lys
 185 190 195
 Ala Leu Gly Cys Arg Lys Ala Met Lys Lys Phe Glu Arg His Thr
 200 205 210
 Leu Leu Glu Tyr Leu Leu Gly Glu Gly Asn Leu Ser Arg Pro Ala
 215 220 225
 Val Gln Leu Leu Gly Asp Val Met Ser Glu Asp Gly Phe Phe Tyr
 230 235 240
 Leu Ser Phe Ala Glu Ala Leu Arg Ala His Ser Cys Leu Ser Asp
 245 250 255
 Arg Leu Gln Tyr Ser Arg Ile Val Gly Gly Trp Asp Leu Leu Pro
 260 265 270
 Arg Ala Leu Leu Ser Ser Leu Ser Gly Leu Val Leu Leu Asn Ala
 275 280 285
 Pro Val Val Ala Met Thr Gln Gly Pro His Asp Val His Val Gln
 290 295 300
 Ile Glu Thr Ser Pro Pro Ala Arg Asn Leu Lys Val Leu Lys Ala
 305 310 315
 Asp Val Val Leu Leu Thr Ala Ser Gly Pro Ala Val Lys Arg Ile
 320 325 330
 Thr Phe Ser Pro Pro Leu Pro Arg His Met Gln Glu Ala Leu Arg
 335 340 345
 Arg Leu His Tyr Val Pro Ala Thr Lys Val Phe Leu Ser Phe Arg
 350 355 360
 Arg Pro Phe Trp Arg Glu Glu His Ile Glu Gly Gly His Ser Asn
 365 370 375
 Thr Asp Arg Pro Ser Arg Met Ile Phe Tyr Pro Pro Pro Arg Glu
 380 385 390
 Gly Ala Leu Leu Leu Ala Ser Tyr Thr Trp Ser Asp Ala Ala Ala
 395 400 405
 Ala Phe Ala Gly Leu Ser Arg Glu Glu Ala Leu Arg Leu Ala Leu
 410 415 420
 Asp Asp Val Ala Ala Leu His Gly Pro Val Val Arg Gln Leu Trp
 425 430 435
 Asp Gly Thr Gly Val Val Lys Arg Trp Ala Glu Asp Gln His Ser
 440 445 450
 Gln Gly Gly Phe Val Val Gln Pro Pro Ala Leu Trp Gln Thr Glu

455	460	465
Lys Asp Asp Trp Thr Val Pro Tyr Gly Arg Ile Tyr Phe Ala Gly		
470	475	480
Glu His Thr Ala Tyr Pro His Gly Trp Val Glu Thr Ala Val Lys		
485	490	495
Ser Ala Leu Arg Ala Ala Ile Lys Ile Asn Ser Arg Lys Gly Pro		
500	505	510
Ala Ser Asp Thr Ala Ser Pro Glu Gly His Ala Ser Asp Met Glu		
515	520	525
Gly Gln Gly His Val His Gly Val Ala Ser Ser Pro Ser His Asp		
530	535	540
Leu Ala Lys Glu Glu Gly Ser His Pro Pro Val Gln Gly Gln Leu		
545	550	555
Ser Leu Gln Asn Thr Thr His Thr Arg Thr Ser His		
560	565	

<210> 85
<211> 3316
<212> DNA
<213> Homo sapiens

<400> 85
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tggaggaacc acgagcgagg gaagaaggac agggactcgt gtggcaggaa 150
gaactcagag ccggaaagcc cccattcact agaagcactg agagatgcgg 200
ccccctcgca gggctgaat ttccctgctgc tgttcacaaa gatgcctttt 250
atctttaact ttttgtttc cccacttccc accccggcgt tgatctgcat 300
cctgacattt ggagctgcca tcttcttggt gctgatcacc agacctcaac 350
ccgtcttacc tcttcttgac ctgaacaatc agtctgtggg aattgaggga 400
ggagcacgga agggggtttc ccagaagaac aatgacctaa caagttgctg 450
cttctcagat gccaagacta tgtatgaggt tttccaaaga ggactcgctg 500
tgtctgacaa tggccctgc ttggatata gaaaaccaa ccagccctac 550
agatggctat cttacaaaca ggtgtctgtat agagcagagt acctgggttc 600
ctgtctcttgc cataaagggtt ataaatcatc accagaccag tttgtcgca 650
tctttgctca gaataggcca gagtggatca tctccgaatt ggcttggtac 700
acgtactcta tggtagctgt acctctgtat gacacccctgg gaccagaagc 750

catcgatcat attgtcaaca aggctgatat cgccatggtg atctgtgaca 800
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ccgagcctga aggtgatcat ccttatggac cccttgcgt atgacctgaa 900
gcaaagaggg gagaagagtg gaattgagat cttatcccta tatgtatgtg 950
agaacctagg caaagagcac ttcagaaaaac ctgtgcctcc tagcccagaa 1000
gacctgagcg tcatctgctt caccagtgg accacaggtg accccaaagg 1050
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gaagaagttc ttgttgaagc tggctgttca cagtaaattc aaagagcttc 1400
aaaagggtat catcaggcat gatagtttctt gggacaagct catcttgca 1450
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gcaccagaga agatagaaaa tatctacaac aggagtcaac cagtgttaca 1950
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agaagacttg cagaaaatttgc gaaagaaag tggccctaaa acttttgaac 2150
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ctcttgacac caacattgaa agcaaagcga ggagagctt ccaaatactt 2250
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aactgatctc cccccccctt ggatttagagt tcctgctcta ctttacccac 3250
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tattacagat aaaaaa 3316

<210> 86
<211> 739
<212> PRT
<213> Homo sapiens

<400> 86
Met Asp Ala Leu Lys Pro Pro Cys Leu Trp Arg Asn His Glu Arg
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Gly Lys Lys Asp Arg Asp Ser Cys Gly Arg Lys Asn Ser Glu Pro
20 25 30

Gly Ser Pro His Ser Leu Glu Ala Leu Arg Asp Ala Ala Pro Ser
 35 40 45
 Gln Gly Leu Asn Phe Leu Leu Leu Phe Thr Lys Met Leu Phe Ile
 50 55 60
 Phe Asn Phe Leu Phe Ser Pro Leu Pro Thr Pro Ala Leu Ile Cys
 65 70 75
 Ile Leu Thr Phe Gly Ala Ala Ile Phe Leu Trp Leu Ile Thr Arg
 80 85 90
 Pro Gln Pro Val Leu Pro Leu Leu Asp Leu Asn Asn Gln Ser Val
 95 100 105
 Gly Ile Glu Gly Gly Ala Arg Lys Gly Val Ser Gln Lys Asn Asn
 110 115 120
 Asp Leu Thr Ser Cys Cys Phe Ser Asp Ala Lys Thr Met Tyr Glu
 125 130 135
 Val Phe Gln Arg Gly Leu Ala Val Ser Asp Asn Gly Pro Cys Leu
 140 145 150
 Gly Tyr Arg Lys Pro Asn Gln Pro Tyr Arg Trp Leu Ser Tyr Lys
 155 160 165
 Gln Val Ser Asp Arg Ala Glu Tyr Leu Gly Ser Cys Leu Leu His
 170 175 180
 Lys Gly Tyr Lys Ser Ser Pro Asp Gln Phe Val Gly Ile Phe Ala
 185 190 195
 Gln Asn Arg Pro Glu Trp Ile Ile Ser Glu Leu Ala Cys Tyr Thr
 200 205 210
 Tyr Ser Met Val Ala Val Pro Leu Tyr Asp Thr Leu Gly Pro Glu
 215 220 225
 Ala Ile Val His Ile Val Asn Lys Ala Asp Ile Ala Met Val Ile
 230 235 240
 Cys Asp Thr Pro Gln Lys Ala Leu Val Leu Ile Gly Asn Val Glu
 245 250 255
 Lys Gly Phe Thr Pro Ser Leu Lys Val Ile Ile Leu Met Asp Pro
 260 265 270
 Phe Asp Asp Asp Leu Lys Gln Arg Gly Glu Lys Ser Gly Ile Glu
 275 280 285
 Ile Leu Ser Leu Tyr Asp Ala Glu Asn Leu Gly Lys Glu His Phe
 290 295 300
 Arg Lys Pro Val Pro Pro Ser Pro Glu Asp Leu Ser Val Ile Cys
 305 310 315
 Phe Thr Ser Gly Thr Thr Gly Asp Pro Lys Gly Ala Met Ile Thr

320	325	330
His Gln Asn Ile Val Ser Asn Ala Ala	Ala Phe Leu Lys Cys Val	
335	340	345
Glu His Ala Tyr Glu Pro Thr Pro Asp Asp	Val Ala Ile Ser Tyr	
350	355	360
Leu Pro Leu Ala His Met Phe Glu Arg	Ile Val Gln Ala Val Val	
365	370	375
Tyr Ser Cys Gly Ala Arg Val Gly Phe	Phe Gln Gly Asp Ile Arg	
380	385	390
Leu Leu Ala Asp Asp Met Lys Thr Leu Lys	Pro Thr Leu Phe Pro	
395	400	405
Ala Val Pro Arg Leu Leu Asn Arg Ile Tyr Asp Lys Val Gln Asn		
410	415	420
Glu Ala Lys Thr Pro Leu Lys Lys Phe	Leu Leu Lys Leu Ala Val	
425	430	435
Ser Ser Lys Phe Lys Glu Leu Gln Lys	Gly Ile Ile Arg His Asp	
440	445	450
Ser Phe Trp Asp Lys Leu Ile Phe Ala Lys	Ile Gln Asp Ser Leu	
455	460	465
Gly Gly Arg Val Arg Val Ile Val Thr	Gly Ala Ala Pro Met Ser	
470	475	480
Thr Ser Val Met Thr Phe Phe Arg Ala Ala	Met Gly Cys Gln Val	
485	490	495
Tyr Glu Ala Tyr Gly Gln Thr Glu Cys	Thr Gly Gly Cys Thr Phe	
500	505	510
Thr Leu Pro Gly Asp Trp Thr Ser Gly His	Val Gly Val Pro Leu	
515	520	525
Ala Cys Asn Tyr Val Lys Leu Glu Asp Val	Ala Asp Met Asn Tyr	
530	535	540
Phe Thr Val Asn Asn Glu Gly Glu Val	Cys Ile Lys Gly Thr Asn	
545	550	555
Val Phe Lys Gly Tyr Leu Lys Asp Pro	Glu Lys Thr Gln Glu Ala	
560	565	570
Leu Asp Ser Asp Gly Trp Leu His Thr	Gly Asp Ile Gly Arg Trp	
575	580	585
Leu Pro Asn Gly Thr Leu Lys Ile Ile Asp Arg	Lys Lys Asn Ile	
590	595	600
Phe Lys Leu Ala Gln Gly Glu Tyr Ile Ala	Pro Glu Lys Ile Glu	
605	610	615

Asn Ile Tyr Asn Arg Ser Gln Pro Val Leu Gln Ile Phe Val His
 620 625 630
 Gly Glu Ser Leu Arg Ser Ser Leu Val Gly Val Val Val Pro Asp
 635 640 645
 Thr Asp Val Leu Pro Ser Phe Ala Ala Lys Leu Gly Val Lys Gly
 650 655 660
 Ser Phe Glu Glu Leu Cys Gln Asn Gln Val Val Arg Glu Ala Ile
 665 670 675
 Leu Glu Asp Leu Gln Lys Ile Gly Lys Glu Ser Gly Leu Lys Thr
 680 685 690
 Phe Glu Gln Val Lys Ala Ile Phe Leu His Pro Glu Pro Phe Ser
 695 700 705
 Ile Glu Asn Gly Leu Leu Thr Pro Thr Leu Lys Ala Lys Arg Gly
 710 715 720
 Glu Leu Ser Lys Tyr Phe Arg Thr Gln Ile Asp Ser Leu Tyr Glu
 725 730 735
 His Ile Gln Asp

<210> 87
 <211> 2725
 <212> DNA
 <213> Homo sapiens

<400> 87
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 ccaggacatt ggtgaccgc caatccggta tggacgactg gaagcccagc 150
 cccctcatca agccctttgg ggctcggaag aagcggagct ggtaccttac 200
 ctggaagtat aaactgacaa accagcgggc cctgcggaga ttctgtcaga 250
 caggggccgt gctttcctg ctggtgactg tcattgtcaa tatcaagttg 300
 atcctggaca ctcggcgagc catcagtgaa gccaatgaag acccagagcc 350
 agagcaagac tatgatgagg ccctaggccg cctggagccc ccacggcgc 400
 gagggcagttgg tccccggcgg gtcctggacg tagaggtgta ttcaagtcgc 450
 agcaaagtat atgtggcagt ggatggcacc acggtgctgg aggatgagggc 500
 ccgggagcag ggccggggca tccatgtcat tgtcctcaac caggccacgg 550
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agacagatgt gccattgagc tcagcagaag aggcaagatg ccactggca 900
gacacagagc tgaaccgtcg ccgcggcgc ttctgcagca aagttgaggg 950
ctatggaagt gtatgcagct gcaaggaccc cacacccatc gagttcagcc 1000
ctgaccact cccagacaac aaggtcctca atgtcctgt ggctgtcatt 1050
gcagggAACCC gaccaatta cctgtacagg atgctgcgt ctctgcttc 1100
agcccagggg gtgtctcctc agatgataac agtttcatt gacggctact 1150
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catactccca tcagcatcaa gaatgccgc gtgtctcagc actacaaggc 1250
cagcctcaact gccactttca acctgtttcc ggaggccaag tttgctgtgg 1300
ttcttggaaaga ggacctggac attgctgtgg atttttcag ttctgcagc 1350
caatccatcc acctactgga ggaggatgac agcctgtact gcatctctgc 1400
ctggaatgac caggggtatg aacacacggc tgaggacca gcactactgt 1450
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tacaaggagg agcttgagcc caagtggcct acaccggaaa agctctggaa 1550
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ggttccaggt gtccagctca ggaatgtgga cagtcgttgc aaagaagctt 1750
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caattttcct ggagccaccc ccaaaggagg agggagcccc aggagcccc 2100

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aaaaaaaaaa aaaaaaaaaa aaaaa 2725

<210> 88
<211> 660
<212> PRT
<213> Homo sapiens

<400> 88
Met Asp Asp Trp Lys Pro Ser Pro Leu Ile Lys Pro Phe Gly Ala
1 5 10 15
Arg Lys Lys Arg Ser Trp Tyr Leu Thr Trp Lys Tyr Lys Leu Thr
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Asn Gln Arg Ala Leu Arg Arg Phe Cys Gln Thr Gly Ala Val Leu
35 40 45
Phe Leu Leu Val Thr Val Ile Val Asn Ile Lys Leu Ile Leu Asp
50 55 60
Thr Arg Arg Ala Ile Ser Glu Ala Asn Glu Asp Pro Glu Pro Glu
65 70 75
Gln Asp Tyr Asp Glu Ala Leu Gly Arg Leu Glu Pro Pro Arg Arg
80 85 90
Arg Gly Ser Gly Pro Arg Arg Val Leu Asp Val Glu Val Tyr Ser
95 100 105
Ser Arg Ser Lys Val Tyr Val Ala Val Asp Gly Thr Thr Val Leu
110 115 120
Glu Asp Glu Ala Arg Glu Gln Gly Arg Gly Ile His Val Ile Val
125 130 135

Leu Asn Gln Ala Thr Gly His Val Met Ala Lys Arg Val Phe Asp
 140 145 150
 Thr Tyr Ser Pro His Glu Asp Glu Ala Met Val Leu Phe Leu Asn
 155 160 165
 Met Val Ala Pro Gly Arg Val Leu Ile Cys Thr Val Lys Asp Glu
 170 175 180
 Gly Ser Phe His Leu Lys Asp Thr Ala Lys Ala Leu Leu Arg Ser
 185 190 195
 Leu Gly Ser Gln Ala Gly Pro Ala Leu Gly Trp Arg Asp Thr Trp
 200 205 210
 Ala Phe Val Gly Arg Lys Gly Gly Pro Val Phe Gly Glu Lys His
 215 220 225
 Ser Lys Ser Pro Ala Leu Ser Ser Trp Gly Asp Pro Val Leu Leu
 230 235 240
 Lys Thr Asp Val Pro Leu Ser Ser Ala Glu Glu Ala Glu Cys His
 245 250 255
 Trp Ala Asp Thr Glu Leu Asn Arg Arg Arg Arg Arg Phe Cys Ser
 260 265 270
 Lys Val Glu Gly Tyr Gly Ser Val Cys Ser Cys Lys Asp Pro Thr
 275 280 285
 Pro Ile Glu Phe Ser Pro Asp Pro Leu Pro Asp Asn Lys Val Leu
 290 295 300
 Asn Val Pro Val Ala Val Ile Ala Gly Asn Arg Pro Asn Tyr Leu
 305 310 315
 Tyr Arg Met Leu Arg Ser Leu Leu Ser Ala Gln Gly Val Ser Pro
 320 325 330
 Gln Met Ile Thr Val Phe Ile Asp Gly Tyr Tyr Glu Glu Pro Met
 335 340 345
 Asp Val Val Ala Leu Phe Gly Leu Arg Gly Ile Gln His Thr Pro
 350 355 360
 Ile Ser Ile Lys Asn Ala Arg Val Ser Gln His Tyr Lys Ala Ser
 365 370 375
 Leu Thr Ala Thr Phe Asn Leu Phe Pro Glu Ala Lys Phe Ala Val
 380 385 390
 Val Leu Glu Glu Asp Leu Asp Ile Ala Val Asp Phe Phe Ser Phe
 395 400 405
 Leu Ser Gln Ser Ile His Leu Leu Glu Glu Asp Asp Ser Leu Tyr
 410 415 420
 Cys Ile Ser Ala Trp Asn Asp Gln Gly Tyr Glu His Thr Ala Glu

425	430	435
Asp Pro Ala Leu Leu Tyr Arg Val Glu	Thr Met Pro Gly Leu	Gly
440	445	450
Trp Val Leu Arg Arg Ser Leu Tyr Lys	Glu Glu Leu Glu Pro	Lys
455	460	465
Trp Pro Thr Pro Glu Lys Leu Trp Asp	Trp Asp Met Trp Met	Arg
470	475	480
Met Pro Glu Gln Arg Arg Gly Arg Glu	Cys Ile Ile Pro Asp	Val
485	490	495
Ser Arg Ser Tyr His Phe Gly Ile Val	Gly Leu Asn Met Asn	Gly
500	505	510
Tyr Phe His Glu Ala Tyr Phe Lys Lys	His Lys Phe Asn Thr	Val
515	520	525
Pro Gly Val Gln Leu Arg Asn Val Asp	Ser Leu Lys Lys Glu	Ala
530	535	540
Tyr Glu Val Glu Val His Arg Leu Leu	Ser Glu Ala Glu Val	Leu
545	550	555
Asp His Ser Lys Asn Pro Cys Glu Asp	Ser Phe Leu Pro Asp	Thr
560	565	570
Glu Gly His Thr Tyr Val Ala Phe Ile	Arg Met Glu Lys Asp	Asp
575	580	585
Asp Phe Thr Thr Trp Thr Gln Leu Ala	Lys Cys Leu His Ile	Trp
590	595	600
Asp Leu Asp Val Arg Gly Asn His Arg	Gly Leu Trp Arg Leu	Phe
605	610	615
Arg Lys Lys Asn His Phe Leu Val Val	Gly Val Pro Ala Ser	Pro
620	625	630
Tyr Ser Val Lys Lys Pro Pro Ser Val	Thr Pro Ile Phe Leu	Glu
635	640	645
Pro Pro Pro Lys Glu Glu Gly Ala Pro Gly	Ala Pro Glu Gln	Thr
650	655	660
<210> 89		
<211> 25		
<212> DNA		
<213> Artificial		
<220>		
<221> Artificial sequence		
<222> 1-25		
<223> Synthetic construct.		
<400> 89		

gatggcaaaa cgtgtgttg acacg 25

<210> 90
<211> 22
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-22
<223> Synthetic construct.

<400> 90
cctcaaccag gccacgggcc ac 22

<210> 91
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-24
<223> Synthetic construct.

<400> 91
cccaggcaga gatgcagtac aggc 24

<210> 92
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-26
<223> Synthetic construct.

<400> 92
cctccagtag gtggatggat tggctc 26

<210> 93
<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-47
<223> Synthetic construct.

<400> 93
ctcacccat gaggtgagg ccatgggtcttccctaac atggtag 47

<210> 94
<211> 3037
<212> DNA
<213> Homo sapiens

<400> 94
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ggatgatttc atctccatta gcctgctgtc tctggctatg ttgggtggat 200
gttacgtggc cggaatcatt cccttggctg ttaatttctc agaggaacga 250
ctgaagctgg tgactgtttt gggtgctggc cttctctgtg gaactgctct 300
ggcagtcatc gtgcctgaag gagtacatgc ccttatgaa gatattctt 350
aggaaaaaca ccaccaagca agtgaacac ataatgtat tgcatacagac 400
aaagcagcag aaaaatcagt tgtccatgaa catgagcaca gccacgacca 450
cacacagctg catgcctata ttgggtttc ctcgttctg ggcttcgtt 500
tcatgttgct ggtggaccag attggtaact cccatgtgca ttctactgac 550
gatccagaag cagcaaggTC tagcaattcc aaaatcacca ccacgctggg 600
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ctacttcaca gaccagtgtc cagttattt tgTTTgtggc aatcatgcta 700
cataaggcac cagctgctt tggactggtt tccttcttga tgcatacgtgg 750
cttagagcgg aatcgaatca gaaagcactt gctggcttt gcattggcag 800
caccagttat gtccatggtg acatacttag gactgagtaa gagcagtaaa 850
gaagcccttt cagaggtgaa cggccacggg gtggccatgc ttttctctgc 900
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aacacatttA cgttgcagtt agctatagac atccattgt gttatcttt 1300
aaaaggccct tgacatTTT cgttttaata tttctcttaa ccctattctc 1350
agggaaagatg gaatttagtt ttaaggaaaa gaggagaact tcataactcac 1400
aatgaaatag tgattatgaa aatacagtgt tctgttaatta agctatgtct 1450

ctttcttctt agtttagagg ctctgctact ttatccattg attttaaca 1500
tggtccac catgtaagac tggtgctta gcatctatgc cacatgcgtt 1550
gatggaaggt catagcaccc actcacttag atgctaaagg tgattctagt 1600
taatctggta tagggtcag gaaaatgata gcaagacaca ttgaaagctc 1650
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Asn Ala Thr Gly Val Ala Met Leu Phe Ser Ala Gly Thr Phe Leu 245	230	235	240
Tyr Val Ala Thr Val His Val Leu Pro Glu Val Gly Gly Ile Gly 260	260	265	270
His Ser His Lys Pro Asp Ala Thr Gly Gly Arg Gly Leu Ser Arg 275		280	285
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Gly Ala Val Glu Leu Lys Lys Asn Glu Phe Gln Gly Glu Leu Glu
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Gln Leu Glu Ser Val Asn Lys Leu Tyr Gln Asp Glu Lys Ala Val
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Leu Val Asn Asn Ile Thr Thr Gly Glu Arg Leu Ile Arg Val Leu
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Gln Asp Gln Leu Lys Thr Leu Gln Arg Asn Tyr Gly Arg Leu Gln
 125 130 135

Gln Asp Val Leu Gln Phe Gln Lys Asn Gln Thr Asn Leu Glu Arg
 140 145 150

Lys Phe Ser Tyr Asp Leu Ser Gln Cys Ile Asn Gln Met Lys Glu
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Val Lys Glu Gln Cys Glu Glu Arg Ile Glu Glu Val Thr Lys Lys
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Gly Asn Glu Ala Val Ala Ser Arg Asp Leu Ser Glu Asn Asn Asp
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Gln Arg Gln Gln Leu Gln Ala Leu Ser Glu Pro Gln Pro Arg Leu
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Asn Val Leu Gly Asn Ser Lys Ser Gln Thr Pro Ala Pro Ser Ser
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<211> 1089

<212> PRT

<213> Homo sapiens

<400> 102

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Thr Arg Leu Glu Leu Thr Asn His Ser Ser Cys Gln Glu Pro Pro
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Gly Pro Gly Ser Leu Pro Trp Gly Ser Gln Gly Lys Pro Gly Ala
50 55 60

Cys Trp Met Ala Ser Arg Phe Ser Arg Val Val Leu Val Leu Ile
65 70 75

Asp Ala Leu Arg Phe Asp Phe Ala Gln Pro Gln His Ser His Val
80 85 90

Pro Arg Glu Pro Pro Val Ser Leu Pro Phe Leu Gly Lys Leu Ser
95 100 105

Ser Leu Gln Arg Ile Leu Glu Ile Gln Pro His His Ala Arg Leu
110 115 120

Tyr Arg Ser Gln Val Asp Pro Pro Thr Thr Thr Met Gln Arg Leu
125 130 135

Lys Ala Leu Thr Thr Gly Ser Leu Pro Thr Phe Ile Asp Ala Gly
140 145 150

Ser Asn Phe Ala Ser His Ala Ile Val Glu Asp Asn Leu Ile Lys
155 160 165

Gln Leu Thr Ser Ala Gly Arg Arg Val Val Phe Met Gly Asp Asp
170 175 180

Thr Trp Lys Asp Leu Phe Pro Gly Ala Phe Ser Lys Ala Phe Phe
185 190 195

Phe Pro Ser Phe Asn Val Arg Asp Leu Asp Thr Val Asp Asn Gly

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215	220	225
Val Leu Ile Ala His	Phe Leu Gly Val Asp His Cys Gly His Lys	
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His Gly Pro His	His Pro Glu Met Ala Lys Lys Leu Ser Gln Met	
245	250	255
Asp Gln Val Ile Gln Gly Leu Val Glu Arg Leu Glu Asn Asp Thr		
260	265	270
Leu Leu Val Val Ala Gly Asp His Gly Met Thr Thr Asn Gly Asp		
275	280	285
His Gly Gly Asp Ser Glu Leu Glu Val Ser Ala Ala Leu Phe Leu		
290	295	300
Tyr Ser Pro Thr Ala Val Phe Pro Ser Thr Pro Pro Glu Glu Pro		
305	310	315
Glu Val Ile Pro Gln Val Ser Leu Val Pro Thr Leu Ala Leu Leu		
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Leu Gly Leu Pro Ile Pro Phe Gly Asn Ile Gly Glu Val Met Ala		
335	340	345
Glu Leu Phe Ser Gly Gly Glu Asp Ser Gln Pro His Ser Ser Ala		
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Leu Ala Gln Ala Ser Ala Leu His Leu Asn Ala Gln Gln Val Ser		
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Arg Phe Leu His Thr Tyr Ser Ala Ala Thr Gln Asp Leu Gln Ala		
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Lys Glu Leu His Gln Leu Gln Asn Leu Phe Ser Lys Ala Ser Ala		
395	400	405
Asp Tyr Gln Trp Leu Leu Gln Ser Pro Lys Gly Ala Glu Ala Thr		
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Leu Pro Thr Val Ile Ala Glu Leu Gln Gln Phe Leu Arg Gly Ala		
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Arg Ala Met Cys Ile Glu Ser Trp Ala Arg Phe Ser Leu Val Arg		
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Pro Leu Leu Leu Thr Pro Val Ala Trp Gly Leu Val Gly Ala Ile		
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 Cys Thr Arg Leu Ala Gly Leu Phe His Arg Cys Pro Glu Glu Thr
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 Val Gly Gly Arg Ala Lys Asn Leu Trp Tyr Gly Ala Cys Val Ala
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 Tyr Gly Asn Leu Lys Ser Pro Glu Pro Pro Met Leu Phe Val Arg
 695 700 705
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 Val Ser Gly Ala Ser Met Val Leu Pro Arg Ala Val Ala Gly Leu
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830	835	840
Thr Leu Leu Ala Phe Pro Leu Leu Leu	Leu His Ala Glu Arg Ile	
845	850	855
Ser Leu Val Phe Leu Leu Leu Phe Leu	Gln Ser Phe Leu Leu Leu	
860	865	870
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875	880	885
Thr Val Pro Trp Gln Ala Val Ser Ala	Trp Ala Leu Met Ala Thr	
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Gln Thr Phe Tyr Ser Thr Gly His Gln	Pro Val Phe Pro Ala Ile	
905	910	915
His Trp His Ala Ala Phe Val Gly Phe	Pro Glu Gly His Gly Ser	
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Cys Thr Trp Leu Pro Ala Leu Leu Val	Gly Ala Asn Thr Phe Ala	
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Ser His Leu Leu Phe Ala Val Gly Cys	Pro Leu Leu Leu Leu Trp	
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Pro Phe Leu Cys Glu Ser Gln Gly Leu	Arg Lys Arg Gln Gln Pro	
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Pro Gly Asn Glu Ala Asp Ala Arg Val	Arg Pro Glu Glu Glu	
980	985	990
Glu Pro Leu Met Glu Met Arg Leu Arg	Asp Ala Pro Gln His Phe	
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Tyr Ala Ala Leu Leu Gln Leu Gly	Tyr Leu Phe Ile Leu	
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Gly Ile Gln Ile Leu Ala Cys Ala Leu	Ala Ala Ser Ile Leu Arg	
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Arg His Leu Met Val Trp Lys Val Phe	Ala Pro Lys Phe Ile Phe	
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Glu Ala Val Gly Phe Ile Val Ser Ser	Val Gly Leu Leu Leu Gly	
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<211> 1743

<212> DNA

<213> Homo sapiens

<400> 103

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gaggaagagc catcgacgac cctggtcgac tggatcccc aaactggcag 1250

gctgtgtatt ctttcgcgtt ccagcttcga ccaggattca gagggctgct 1300
agccttcgtt gggggatggg ctcggagagg agggcttct atcttagactc 1350
tatgaggagc cggccacaga caggccacca ggagaaaatg aaacctatct 1400
catgcaattc atggaggaat gggggttata tgtgcagatg gaaaactgat 1450
gccaacactt cctttgcct tttgttcct gtgcaaaca gtgagtcacc 1500
ccttgatcc cagccataaa gtacctggga tgaaagaagt ttttccagt 1550
ttgtcagtgt ctgtgagaat tacttatttc ttttctctat tctcatagca 1600
cgtgtgtat ttgttcatgc atgttaggtct cttaacaatg atggtggcc 1650
tctggagtcc aggggctggc cggttgttct atgcagagaa agcagtcaat 1700
aaatgtttgc cagactgggt gcagaattta ttcaagggtggg tgt 1743

<210> 104

<211> 442

<212> PRT

<213> Homo sapiens

<400> 104

Met	Ser	Tyr	Asn	Gly	Leu	His	Gln	Arg	Val	Phe	Lys	Glu	Leu	Lys
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Leu	Leu	Thr	Leu	Cys	Ser	Ile	Ser	Ser	Gln	Ile	Gly	Pro	Pro	Glu
				20					25				30	
Val	Ala	Leu	Thr	Thr	Asp	Glu	Lys	Ser	Ile	Ser	Val	Val	Leu	Thr
				35					40				45	
Ala	Pro	Glu	Lys	Trp	Lys	Arg	Asn	Pro	Glu	Asp	Leu	Pro	Val	Ser
				50					55				60	
Met	Gln	Gln	Ile	Tyr	Ser	Asn	Leu	Lys	Tyr	Asn	Val	Ser	Val	Leu
				65					70				75	
Asn	Thr	Lys	Ser	Asn	Arg	Thr	Trp	Ser	Gln	Cys	Val	Thr	Asn	His
				80					85				90	
Thr	Leu	Val	Leu	Thr	Trp	Leu	Glu	Pro	Asn	Thr	Leu	Tyr	Cys	Val
				95					100				105	
His	Val	Glu	Ser	Phe	Val	Pro	Gly	Pro	Pro	Arg	Arg	Ala	Gln	Pro
				110					115				120	
Ser	Glu	Lys	Gln	Cys	Ala	Arg	Thr	Leu	Lys	Asp	Gln	Ser	Ser	Glu
				125					130				135	
Phe	Lys	Ala	Lys	Ile	Ile	Phe	Trp	Tyr	Val	Leu	Pro	Ile	Ser	Ile
				140					145				150	
Thr	Val	Phe	Leu	Phe	Ser	Val	Met	Gly	Tyr	Ser	Ile	Tyr	Arg	Tyr
				155					160				165	

Ile His Val Gly Lys Glu Lys His Pro Ala Asn Leu Ile Leu Ile
 170 175 180
 Tyr Gly Asn Glu Phe Asp Lys Arg Phe Phe Val Pro Ala Glu Lys
 185 190 195
 Ile Val Ile Asn Phe Ile Thr Leu Asn Ile Ser Asp Asp Ser Lys
 200 205 210
 Ile Ser His Gln Asp Met Ser Leu Leu Gly Lys Ser Ser Asp Val
 215 220 225
 Ser Ser Leu Asn Asp Pro Gln Pro Ser Gly Asn Leu Arg Pro Pro
 230 235 240
 Gln Glu Glu Glu Glu Val Lys His Leu Gly Tyr Ala Ser His Leu
 245 250 255
 Met Glu Ile Phe Cys Asp Ser Glu Glu Asn Thr Glu Gly Thr Ser
 260 265 270
 Leu Thr Gln Gln Glu Ser Leu Ser Arg Thr Ile Pro Pro Asp Lys
 275 280 285
 Thr Val Ile Glu Tyr Glu Tyr Asp Val Arg Thr Thr Asp Ile Cys
 290 295 300
 Ala Gly Pro Glu Glu Gln Glu Leu Ser Leu Gln Glu Glu Val Ser
 305 310 315
 Thr Gln Gly Thr Leu Leu Glu Ser Gln Ala Ala Leu Ala Val Leu
 320 325 330
 Gly Pro Gln Thr Leu Gln Tyr Ser Tyr Thr Pro Gln Leu Gln Asp
 335 340 345
 Leu Asp Pro Leu Ala Gln Glu His Thr Asp Ser Glu Glu Gly Pro
 350 355 360
 Glu Glu Glu Pro Ser Thr Thr Leu Val Asp Trp Asp Pro Gln Thr
 365 370 „ 375
 Gly Arg Leu Cys Ile Pro Ser Leu Ser Ser Phe Asp Gln Asp Ser
 380 385 390
 Glu Gly Cys Glu Pro Ser Glu Gly Asp Gly Leu Gly Glu Glu Gly
 395 400 405
 Leu Leu Ser Arg Leu Tyr Glu Glu Pro Ala Pro Asp Arg Pro Pro
 410 415 420
 Gly Glu Asn Glu Thr Tyr Leu Met Gln Phe Met Glu Glu Trp Gly
 425 430 435
 Leu Tyr Val Gln Met Glu Asn
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<210> 105

<211> 21
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-21
<223> Synthetic construct

<400> 105
cgctgctgct gttgctcctg g .21

<210> 106
<211> 18
<212> DNA
<213> Artificial

<220>
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<222> 1-18
<223> Synthetic construct.

<400> 106
cagtgtgcc a ggactttg 18

<210> 107
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 107
agtcgcaggc a gcgttgg 18

<210> 108
<211> 25
<212> DNA
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<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 108
ctcctccgag t ctgtgtgct cctgc 25

<210> 109
<211> 51
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence

<222> 1-51
<223> Synthetic construct.

<400> 109
ggacggcag ttccctgtgt ctctggtgtt ttgcctaaac ctgcaaacat 50
c 51

<210> 110
<211> 1114
<212> DNA
<213> Homo sapiens

<400> 110
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cgccagcctg cgtctgccat ggggctcggtt ttgaggggctt gggacgtcc 100
tctgctgact gtggccaccg ccctgatgct gccgtgaag ccccccgcag 150
gctcctgggg ggcccagatc atcggggggcc acgaggtgac cccccactcc 200
aggccctaca tggcatccgt gcgcattcggtt ggccaacatc actgcggagg 250
cttcctgctg cgagcccgctt ggggtgtctc ggccggccac tgcttcagcc 300
acagagacct ccgcactggc ctgggtggtgc tggcgccca cgtcctgagt 350
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tgcaaaggc agaagcaaac ccagtaaaat gttaactgac aaaaaaaaaaa 1100

aaaaaaaaaa gaaa 1114

<210> 111

<211> 283

<212> PRT

<213> Homo sapiens

<400> 111

Met Gly Leu Gly Leu Arg Gly Trp Gly Arg Pro Leu Leu Thr Val
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Ala Thr Ala Leu Met Leu Pro Val Lys Pro Pro Ala Gly Ser Trp
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Gly Ala Gln Ile Ile Gly Gly His Glu Val Thr Pro His Ser Arg
35 40 45

Pro Tyr Met Ala Ser Val Arg Phe Gly Gly Gln His His Cys Gly
50 55 60

Gly Phe Leu Leu Arg Ala Arg Trp Val Val Ser Ala Ala His Cys
65 70 75

Phe Ser His Arg Asp Leu Arg Thr Gly Leu Val Val Leu Gly Ala
80 85 90

His Val Leu Ser Thr Ala Glu Pro Thr Gln Gln Val Phe Gly Ile
95 100 105

Asp Ala Leu Thr Thr His Pro Asp Tyr His Pro Met Thr His Ala
110 115 120

Asn Asp Ile Cys Leu Leu Arg Leu Asn Gly Ser Ala Val Leu Gly
125 130 135

Pro Ala Val Gly Leu Leu Arg Leu Pro Gly Arg Arg Ala Arg Pro
140 145 150

Pro Thr Ala Gly Thr Arg Cys Arg Val Ala Gly Trp Gly Phe Val
155 160 165

Ser Asp Phe Glu Glu Leu Pro Pro Gly Leu Met Glu Ala Lys Val
170 175 180

Arg Val Leu Asp Pro Asp Val Cys Asn Ser Ser Trp Lys Gly His
185 190 195

Leu Thr Leu Thr Met Leu Cys Thr Arg Ser Gly Asp Ser His Arg
200 205 210

Arg Gly Phe Cys Ser Ala Asp Ser Gly Gly Pro Leu Val Cys Arg
215 220 225

Asn Arg Ala His Gly Leu Val Ser Phe Ser Gly Leu Trp Cys Gly
230 235 240

Asp Pro Lys Thr Pro Asp Val Tyr Thr Gln Val Ser Ala Phe Val
245 250 255

Ala Trp Ile Trp Asp Val Val Arg Arg Ser Ser Pro Gln Pro Gly
260 265 270

Pro Leu Pro Gly Thr Thr Arg Pro Pro Gly Glu Ala Ala
275 280

<210> 112
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 112
gacgtctgca acagctcctg gaag 24

<210> 113
<211> 23
<212> DNA
<213> Artificial

<220>
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<222> 1-23
<223> Synthetic construct.

<400> 113
cgagaaggaa acgaggccgt gag 23

<210> 114
<211> 44
<212> DNA
<213> Artificial

<220>
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<222> 1-44
<223> Synthetic construct.

<400> 114
tgacacttac catgctctgc acccgcatgt gggacagcca caga 44

<210> 115
<211> 1808
<212> DNA
<213> Homo sapiens

<400> 115
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cgctgtcggc gctgggcacg gtagcaggcg ccgccgtgct gctcaaggac 150
tatgtcacccg gtggggcttg cccccagcaag gccaccatcc ctggaaagac 200

ggtcatcgta acgggcgcca acacaggcat cgggaagcag accgccttgg 250
aactggccag gagaggaggc aacatcatcc tggcctgccg agacatggag 300
aagtgtgagg cggcagcaaa ggacatccgc ggggagaccc tcaatcacca 350
tgtcaacgcc cggcacctgg acttggcttc cctcaagtct atccgagagt 400
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gctcattt 1808

<210> 116
<211> 331
<212> PRT
<213> Homo sapiens

<400> 116
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20 25 30
Pro Ser Lys Ala Thr Ile Pro Gly Lys Thr Val Ile Val Thr Gly
35 40 45
Ala Asn Thr Gly Ile Gly Lys Gln Thr Ala Leu Glu Leu Ala Arg
50 55 60
Arg Gly Gly Asn Ile Ile Leu Ala Cys Arg Asp Met Glu Lys Cys
65 70 75
Glu Ala Ala Ala Lys Asp Ile Arg Gly Glu Thr Leu Asn His His
80 85 90
Val Asn Ala Arg His Leu Asp Leu Ala Ser Leu Lys Ser Ile Arg
95 100 105
Glu Phe Ala Ala Lys Ile Ile Glu Glu Glu Glu Arg Val Asp Ile
110 115 120
Leu Ile Asn Asn Ala Gly Val Met Arg Cys Pro His Trp Thr Thr
125 130 135
Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His
140 145 150
Phe Leu Leu Thr Asn Leu Leu Asp Lys Leu Lys Ala Ser Ala
155 160 165
Pro Ser Arg Ile Ile Asn Leu Ser Ser Leu Ala His Val Ala Gly
170 175 180
His Ile Asp Phe Asp Asp Leu Asn Trp Gln Thr Arg Lys Tyr Asn
185 190 195
Thr Lys Ala Ala Tyr Cys Gln Ser Lys Leu Ala Ile Val Leu Phe
200 205 210
Thr Lys Glu Leu Ser Arg Arg Leu Gln Gly Ser Gly Val Thr Val
215 220 225

Asn	Ala	Leu	His	Pro	Gly	Val	Ala	Arg	Thr	Glu	Leu	Gly	Arg	His
									230	235				240
Thr	Gly	Ile	His	Gly	Ser	Thr	Phe	Ser	Ser	Thr	Thr	Leu	Gly	Pro
									245	250				255
Ile	Phe	Trp	Leu	Leu	Val	Lys	Ser	Pro	Glu	Leu	Ala	Ala	Gln	Pro
						260			265					270
Ser	Thr	Tyr	Leu	Ala	Val	Ala	Glu	Glu	Leu	Ala	Asp	Val	Ser	Gly
						275			280					285
Lys	Tyr	Phe	Asp	Gly	Leu	Lys	Gln	Lys	Ala	Pro	Ala	Pro	Glu	Ala
						290			295					300
Glu	Asp	Glu	Glu	Val	Ala	Arg	Arg	Leu	Trp	Ala	Glu	Ser	Ala	Arg
						305			310					315
Leu	Val	Gly	Leu	Glu	Ala	Pro	Ser	Val	Arg	Glu	Gln	Pro	Leu	Pro
						320			325					330

Arg

<210>	117				
<211>	2249				
<212>	DNA				
<213>	Homo sapiens				
<400>	117				
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gggcgacacg	ttctcgccgc	tgaccagcgt	ggcgcgcgcc	ctggcgcccg	150
agcgcggct	gctggggctg	ctgaggcggt	acctgcgcgg	ggaggaggcg	200
cggctgcggg	acctgactag	attctacgac	aaggtaactt	ctttgcata	250
ggattcaaca	accctgtgg	ctaaccctct	gcttgcat	actctcatca	300
aacgcctgca	gtctgactgg	aggaatgtgg	tacatagtct	ggaggccagt	350
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ttctctcaca	ggggatgact	gcttcca	tgcaagg	gcctatgaca	600
tgggggat	ttaccatgcc	attccatggc	tggaggaggc	tgtcagtctc	650
ttccgaggat	cttacggaga	gtgaaagaca	gaggatgagg	caagtctaga	700

agatgccttg gatcacttgg cctttgctta tttccggca ggaaatgtt 750
cgtgtccct cagcctctc cgggagttc ttctctacag cccagataat 800
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acctgcagac cagagacacc tacgagggc tatgtcagac cctgggttcc 950
cagcccactc tctaccagat ccctagcctc tactgttcct atgagaccaa 1000
ttccaacgcc tacctgctgc tccagccat ccggaaggag gtcatccacc 1050
tggagcccta cattgctctc taccatgact tcgtcagtga ctcagaggct 1100
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agccacggaa gtcagagtag gatgcacagt acaaaggagg ggggagtgga 1900
ggcctgagag ggaagtttct ggagttcaga tactctctgt tgggaacagg 1950
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cttgaccaca gggaccaaga agtggcaatg aggacacactg caggagggc 2050
tagcctgact cccagaactt taagacttgc tccccactgc cttctgctgc 2100
agcccaagca gggagtgtcc ccctcccaga agcatatccc agatgagtgg 2150

tacattatat aaggatttt ttaagttga aaacaacttt ctttcttt 2200
 tgtatgtgg tttaaca cagtcattaa aaatgttat aaatcaaaa 2249
 <210> 118
 <211> 544
 <212> PRT
 <213> Homo sapiens
 <400> 118
 Met Gly Pro Gly Ala Arg Leu Ala Ala Leu Leu Ala Val Leu Ala
 1 5 10 15
 Leu Gly Thr Gly Asp Pro Glu Arg Ala Ala Ala Arg Gly Asp Thr
 20 25 30
 Phe Ser Ala Leu Thr Ser Val Ala Arg Ala Leu Ala Pro Glu Arg
 35 40 45
 Arg Leu Leu Gly Leu Leu Arg Arg Tyr Leu Arg Gly Glu Glu Ala
 50 55 60
 Arg Leu Arg Asp Leu Thr Arg Phe Tyr Asp Lys Val Leu Ser Leu
 65 70 75
 His Glu Asp Ser Thr Thr Pro Val Ala Asn Pro Leu Leu Ala Phe
 80 85 90
 Thr Leu Ile Lys Arg Leu Gln Ser Asp Trp Arg Asn Val Val His
 95 100 105
 Ser Leu Glu Ala Ser Glu Asn Ile Arg Ala Leu Lys Asp Gly Tyr
 110 115 120
 Glu Lys Val Glu Gln Asp Leu Pro Ala Phe Glu Asp Leu Glu Gly
 125 130 135
 Ala Ala Arg Ala Leu Met Arg Leu Gln Asp Val Tyr Met Leu Asn
 140 145 150
 Val Lys Gly Leu Ala Arg Gly Val Phe Gln Arg Val Thr Gly Ser
 155 160 165
 Ala Ile Thr Asp Leu Tyr Ser Pro Lys Arg Leu Phe Ser Leu Thr
 170 175 180
 Gly Asp Asp Cys Phe Gln Val Gly Lys Val Ala Tyr Asp Met Gly
 185 190 195
 Asp Tyr Tyr His Ala Ile Pro Trp Leu Glu Glu Ala Val Ser Leu
 200 205 210
 Phe Arg Gly Ser Tyr Gly Glu Trp Lys Thr Glu Asp Glu Ala Ser
 215 220 225
 Leu Glu Asp Ala Leu Asp His Leu Ala Phe Ala Tyr Phe Arg Ala
 230 235 240

Gly Asn Val Ser Cys Ala Leu Ser Leu Ser Arg Glu Phe Leu Leu
 245 250 255
 Tyr Ser Pro Asp Asn Lys Arg Met Ala Arg Asn Val Leu Lys Tyr
 260 265 270
 Glu Arg Leu Leu Ala Glu Ser Pro Asn His Val Val Ala Glu Ala
 275 280 285
 Val Ile Gln Arg Pro Asn Ile Pro His Leu Gln Thr Arg Asp Thr
 290 295 300
 Tyr Glu Gly Leu Cys Gln Thr Leu Gly Ser Gln Pro Thr Leu Tyr
 305 310 315
 Gln Ile Pro Ser Leu Tyr Cys Ser Tyr Glu Thr Asn Ser Asn Ala
 320 325 330
 Tyr Leu Leu Leu Gln Pro Ile Arg Lys Glu Val Ile His Leu Glu
 335 340 345
 Pro Tyr Ile Ala Leu Tyr His Asp Phe Val Ser Asp Ser Glu Ala
 350 355 360
 Gln Lys Ile Arg Glu Leu Ala Glu Pro Trp Leu Gln Arg Ser Val
 365 370 375
 Val Ala Ser Gly Glu Lys Gln Leu Gln Val Glu Tyr Arg Ile Ser
 380 385 390
 Lys Ser Ala Trp Leu Lys Asp Thr Val Asp Pro Lys Leu Val Thr
 395 400 405
 Leu Asn His Arg Ile Ala Ala Leu Thr Gly Leu Asp Val Arg Pro
 410 415 420
 Pro Tyr Ala Glu Tyr Leu Gln Val Val Asn Tyr Gly Ile Gly Gly
 425 430 435
 His Tyr Glu Pro His Phe Asp His Ala Thr Ser Pro Ser Ser Pro
 440 445 450
 Leu Tyr Arg Met Lys Ser Gly Asn Arg Val Ala Thr Phe Met Ile
 455 460 465
 Tyr Leu Ser Ser Val Glu Ala Gly Gly Ala Thr Ala Phe Ile Tyr
 470 475 480
 Ala Asn Leu Ser Val Pro Val Val Arg Asn Ala Ala Leu Phe Trp
 485 490 495
 Trp Asn Leu His Arg Ser Gly Glu Gly Asp Ser Asp Thr Leu His
 500 505 510
 Ala Gly Cys Pro Val Leu Val Gly Asp Lys Trp Val Ala Asn Lys
 515 520 525
 Trp Ile His Glu Tyr Gly Gln Glu Phe Arg Arg Pro Cys Ser Ser

530

535

540

Ser Pro Glu Asp

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<210> 119
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 119
cgggacagga gaccagaaa ggg 23

<210> 120
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 120
ggccaagtga tccaaaggcat cttc 24

<210> 121
<211> 49
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-49
<223> Synthetic construct.

<400> 121
ctgcgggacc tgactagatt ctacgacaag gtactttctt tgcatgggg 49

<210> 122
<211> 1778
<212> DNA
<213> Homo sapiens

<400> 122
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gaatcggccc tggcaggtgg ggccacgagc gctggctgag ggaccgagcc 150
ggagagcccc ggagcccccg taacccgcgc ggggagcgcc caggatgccc 200
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ccctggtcct gtctgtgggc atctatgcag aggttgagcg gcagaaatat 350
aaaacccttg aaagtgcctt cctggctcca gccatcatcc tcataccct 400
gggcgtcgac atgttcatgg tctccttcat tggtgtgctg gcgtccctcc 450
gtgacaacct gtaccttctc caagcattca tgtacatcct tggatctgc 500
ctcatcatgg agctcattgg tggcgtggtg gccttgaccc tccggAACCA 550
gaccattgac ttcttgaacg acaacattcg aagaggaatt gagaactact 600
atgatgatct ggacttcaaa aacatcatgg actttgttca gaaaaagttc 650
aagtgtgtg gcggggagga ctaccgagat tggagcaaga atcagtagcca 700
cgactgcagt gcccctggac ccctggcctg tgggtgccc tacacctgct 750
gcatcaggaa cacgacagaa gttgtcaaca ccatgtgtgg ctacaaaact 800
atcgacaagg agcgttttag tttgcaggat gtcatctacg tgccgggctg 850
caccaacgcc gtgatcatct gtttcatgga caactacacc atcatggcgt 900
gcatttcctt gggcatcctg cttccccagt tcctgggggt gctgctgacg 950
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cttttctcag cctccctagg gccttgagcc ctcttgcaag ggcggctgct 1600
tccttgagcc tagttttttt ttacgtgatt tttgttaacat tcattttttt 1650

gtacagataa caggagtttc tgactaatca aagctggat ttcccccgtat 1700
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 catgttttgt tttgtttta aaaaaaaaa 1778

 <210> 123
 <211> 294
 <212> PRT
 <213> Homo sapiens

 <400> 123
 Met Pro Arg Gly Asp Ser Glu Gln Val Arg Tyr Cys Ala Arg Phe
 1 5 10 15
 Ser Tyr Leu Trp Leu Lys Phe Ser Leu Ile Ile Tyr Ser Thr Val
 20 25 30
 Phe Trp Leu Ile Gly Ala Leu Val Leu Ser Val Gly Ile Tyr Ala
 35 40 45
 Glu Val Glu Arg Gln Lys Tyr Lys Thr Leu Glu Ser Ala Phe Leu
 50 55 60
 Ala Pro Ala Ile Ile Leu Ile Leu Gly Val Val Met Phe Met
 65 70 75
 Val Ser Phe Ile Gly Val Leu Ala Ser Leu Arg Asp Asn Leu Tyr
 80 85 90
 Leu Leu Gln Ala Phe Met Tyr Ile Leu Gly Ile Cys Leu Ile Met
 95 100 105
 Glu Leu Ile Gly Gly Val Val Ala Leu Thr Phe Arg Asn Gln Thr
 110 115 120
 Ile Asp Phe Leu Asn Asp Asn Ile Arg Arg Gly Ile Glu Asn Tyr
 125 130 135
 Tyr Asp Asp Leu Asp Phe Lys Asn Ile Met Asp Phe Val Gln Lys
 140 145 150
 Lys Phe Lys Cys Cys Gly Gly Glu Asp Tyr Arg Asp Trp Ser Lys
 155 160 165
 Asn Gln Tyr His Asp Cys Ser Ala Pro Gly Pro Leu Ala Cys Gly
 170 175 180
 Val Pro Tyr Thr Cys Cys Ile Arg Asn Thr Thr Glu Val Val Asn
 185 190 195
 Thr Met Cys Gly Tyr Lys Thr Ile Asp Lys Glu Arg Phe Ser Val
 200 205 210
 Gln Asp Val Ile Tyr Val Arg Gly Cys Thr Asn Ala Val Ile Ile
 215 220 225
 Trp Phe Met Asp Asn Tyr Thr Ile Met Ala Cys Ile Leu Leu Gly

230	235	240
Ile Leu Leu Pro Gln Phe Leu Gly Val	Leu Leu Thr Leu Leu Tyr	
245	250	255
Ile Thr Arg Val Glu Asp Ile Ile Met	Glu His Ser Val Thr Asp	
260	265	270
Gly Leu Leu Gly Pro Gly Ala Lys Pro	Ser Val Glu Ala Ala Gly	
275	280	285
Thr Gly Cys Cys Leu Cys Tyr Pro Asn		
290		

<210> 124
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 124
atcatctatt ccaccgtgtt ctggc 25

<210> 125
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 125
gacagagtgc tccatgatga tgtcc 25

<210> 126
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 126
cctgtctgtg ggcatctatg cagagggttga gcggcagaaa tataaaaccc 50

<210> 127
<211> 1636
<212> DNA
<213> Homo sapiens

<400> 127
gaggagcggg ccgaggactc cagcgtcccc aggtctggca tcctgcac 50
gctgccotct gacacctggg aagatggccg gcccgtggac cttcaccc 100
ctctgtggtt tgctggcagc caccttgate caagccaccc tcaatccc 150
tgcaatcttc atccctcgcc caaaaagtcat caaaagaaag ctgacacagg 200
agctgaagga ccacaacgcc accagcatcc tgcaatgcgt gcccgtgctc 250
agtgcacatgc gggaaaagcc agccggaggc atccctgtgc tggcagcct 300
ggtaaacacc gtccatgc acatcatctg gctgaaggc atcacagcta 350
acatcccca gctgcaggta aagccctcg ccaatgacca ggagctgcta 400
gtcaagatcc ccctggacat ggtggctgga ttcaacacgc ccctggtaa 450
gaccatcgta gagttccaca tgacactga ggcccaagcc accatccca 500
tggacaccag tgcaagtggc cccacccggc tggcctcag tgactgtgcc 550
accagccatg ggagcctgcg catccaaactg ctgtataagc tctccctcct 600
ggtaacgcc ttagctaagc aggtcatgaa cctccatgtg ccattccctgc 650
ccaatctagt gaaaaaccag ctgtgtcccc tgatcgaggc ttccttcaat 700
ggcatgtatg cagacccct gcagctggta aaggtgccc tttccctcag 750
cattgaccgt ctggagttt accttctgtta tcctgcccacc aagggtgaca 800
ccattcagct ctacccgggg gccaagttgt tggactcaca gggaaagggt 850
accaagtggc tcaataactc tgcaatcc tcgacaaatgc ccaccctgga 900
caacatcccc ttcagccatca tcgtgagtc ggacgtggta aaagctgcag 950
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aggacactcc cgagttttt atagaccaag gccatgccaa ggtggcccaa 1150
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caactgagatc atccactcca tcctgctgcc gaaccagaat ggcaaattaa 1400
gatctggggc cccagtgta ttggtaagg ctttgggatt cgaggcagct 1450

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 cctctctgca atcaataaac acttgcctgt gaaaaa 1636

<210> 128
 <211> 484
 <212> PRT
 <213> Homo sapiens

<400> 128
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 20 25 30

Leu Gly Pro Lys Val Ile Lys Glu Lys Leu Thr Gln Glu Leu Lys
 35 40 45

Asp His Asn Ala Thr Ser Ile Leu Gln Gln Leu Pro Leu Leu Ser
 50 55 60

Ala Met Arg Glu Lys Pro Ala Gly Gly Ile Pro Val Leu Gly Ser
 65 70 75

Leu Val Asn Thr Val Leu Lys His Ile Ile Trp Leu Lys Val Ile
 80 85 90

Thr Ala Asn Ile Leu Gln Leu Gln Val Lys Pro Ser Ala Asn Asp
 95 100 105

Gln Glu Leu Leu Val Lys Ile Pro Leu Asp Met Val Ala Gly Phe
 110 115 120

Asn Thr Pro Leu Val Lys Thr Ile Val Glu Phe His Met Thr Thr
 125 130 135

Glu Ala Gln Ala Thr Ile Arg Met Asp Thr Ser Ala Ser Gly Pro
 140 145 150

Thr Arg Leu Val Leu Ser Asp Cys Ala Thr Ser His Gly Ser Leu
 155 160 165

Arg Ile Gln Leu Leu Tyr Lys Leu Ser Phe Leu Val Asn Ala Leu
 170 175 180

Ala Lys Gln Val Met Asn Leu Leu Val Pro Ser Leu Pro Asn Leu
 185 190 195

Val Lys Asn Gln Leu Cys Pro Val Ile Glu Ala Ser Phe Asn Gly
 200 205 210

Met Tyr Ala Asp Leu Leu Gln Leu Val Lys Val Pro Ile Ser Leu
 215 220 225

Ser Ile Asp Arg Leu Glu Phe Asp Leu Leu Tyr Pro Ala Ile Lys
 230 235 240
 Gly Asp Thr Ile Gln Leu Tyr Leu Gly Ala Lys Leu Leu Asp Ser
 245 250 255
 Gln Gly Lys Val Thr Lys Trp Phe Asn Asn Ser Ala Ala Ser Leu
 260 265 270
 Thr Met Pro Thr Leu Asp Asn Ile Pro Phe Ser Leu Ile Val Ser
 275 280 285
 Gln Asp Val Val Lys Ala Ala Val Ala Ala Val Leu Ser Pro Glu
 290 295 300
 Glu Phe Met Val Leu Leu Asp Ser Val Leu Pro Glu Ser Ala His
 305 310 315
 Arg Leu Lys Ser Ser Ile Gly Leu Ile Asn Glu Lys Ala Ala Asp
 320 325 330
 Lys Leu Gly Ser Thr Gln Ile Val Lys Ile Leu Thr Gln Asp Thr
 335 340 345
 Pro Glu Phe Phe Ile Asp Gln Gly His Ala Lys Val Ala Gln Leu
 350 355 360
 Ile Val Leu Glu Val Phe Pro Ser Ser Glu Ala Leu Arg Pro Leu
 365 370 375
 Phe Thr Leu Gly Ile Glu Ala Ser Ser Glu Ala Gln Phe Tyr Thr
 380 385 390
 Lys Gly Asp Gln Leu Ile Leu Asn Leu Asn Asn Ile Ser Ser Asp
 395 400 405
 Arg Ile Gln Leu Met Asn Ser Gly Ile Gly Trp Phe Gln Pro Asp
 410 415 420
 Val Leu Lys Asn Ile Ile Thr Glu Ile Ile His Ser Ile Leu Leu
 425 430 435
 Pro Asn Gln Asn Gly Lys Leu Arg Ser Gly Val Pro Val Ser Leu
 440 445 450
 Val Lys Ala Leu Gly Phe Glu Ala Ala Glu Ser Ser Leu Thr Lys
 455 460 465
 Asp Ala Leu Val Leu Thr Pro Ala Ser Leu Trp Lys Pro Ser Ser
 470 475 480
 Pro Val Ser Gln

<210> 129
 <211> 2213
 <212> DNA
 <213> Homo sapiens

<400> 129
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aaagaaggag atggtgttat ctgaaaaggt tagtcagctg atggaatgga 150
ctaacaaaag acctgtataa agaatgaatg gagacaagtt ccgtcgccct 200
gtgaaagccc caccgagaaa ttactccgtt atcgtcatgt tcactgctct 250
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agatcctggc aaactcctgg cgatactcca gtgcattcac caacaggata 350
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aaacatgaat tcagctccaa ctttcatcaa ctttcctgca aaaggaaac 450
ccaaacgggg tgatacatat gagttacagg tgcggggttt ttcagctgag 500
cagattgccc ggtggatcgc cgacagaact gatgtcaata ttagagtatgat 550
tagacccca aattatgctg gtcccccattt gttgggattt cttttggctg 600
ttattggtgg acttgtgtat cttcgaagaa gtaatatgga atttctctt 650
aataaaactg gatgggctt tgcaagttt tggtttgtgc ttgctatgac 700
atctggtcaa atgtggAACC atataagagg accaccatat gcccataaga 750
atccccacac gggacatgtg aattatatcc atggaagcag tcaagccag 800
ttttagctg aaacacacat tttttttctg tttatggtg gagttacatt 850
aggaatggtg cttttatgtg aagctgctac ctctgacatg gatattggaa 900
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ctttctgatg agttaaaaag gtcccaagaga tatatacaca ctggagttact 1050
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tttatggAACC atttaattttt gtacaattaa gtatattata aaaattgtaa 1300
aactactact ttgttttagt tagaacaagacta ctcaaaaacta ctttagttaa 1350
cttggtcattc tgattttata ttgccttata caaagatggg gaaagtaagt 1400
cctgaccagg tgttccaca tatgcctgtt acagataact acattaggaa 1450

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gaacaccatt cttagagca cacgtctagc cctcagcaag acagttgttt 1600
ctccctccctt ttgcataattt cctactgcgc tccagcctga gtgatagagt 1650
gagactctgt ctcaaaaaaa agtatctcta aatacaggat tataatttct 1700
gcttgagtat ggtgttaact accttgtatt tagaaagatt tcagattcat 1750
tccatctcct tagtttctt ttaaggtgac ccacatgtga taaaaatata 1800
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cagttagaaa aggactccct ggccaggcgc agtgacttac gcctgtaatc 1950
tcagcacttt gggaggccaa ggcaggcaga tcacgaggc aggagttcga 2000
gaccatcctg gccaacatgg tcaaaccgg tctctactaa aaatataaaa 2050
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agatcacgcc actgcactcc agcctggcaa cagagcgaga ctccatctca 2200
aaaaaaaaaa aaa 2213

<210> 130

<211> 335

<212> PRT

<213> Homo sapiens

<400> 130

Met	Ala	Ala	Arg	Trp	Arg	Phe	Trp	Cys	Val	Ser	Val	Thr	Met	Val
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Val	Ala	Leu	Leu	Ile	Val	Cys	Asp	Val	Pro	Ser	Ala	Ser	Ala	Gln
				20					25				30	
Arg	Lys	Lys	Glu	Met	Val	Leu	Ser	Glu	Lys	Val	Ser	Gln	Leu	Met
				35				40				45		
Glu	Trp	Thr	Asn	Lys	Arg	Pro	Val	Ile	Arg	Met	Asn	Gly	Asp	Lys
				50				55				60		
Phe	Arg	Arg	Leu	Val	Lys	Ala	Pro	Pro	Arg	Asn	Tyr	Ser	Val	Ile
				65				70				75		
Val	Met	Phe	Thr	Ala	Leu	Gln	Leu	His	Arg	Gln	Cys	Val	Val	Cys
				80				85				90		
Lys	Gln	Ala	Asp	Glu	Glu	Phe	Gln	Ile	Leu	Ala	Asn	Ser	Trp	Arg
				95				100				105		

Tyr	Ser	Ser	Ala	Phe	Thr	Asn	Arg	Ile	Phe	Phe	Ala	Met	Val	Asp
110								115						120
Phe	Asp	Glu	Gly	Ser	Asp	Val	Phe	Gln	Met	Leu	Asn	Met	Asn	Ser
125								130						135
Ala	Pro	Thr	Phe	Ile	Asn	Phe	Pro	Ala	Lys	Gly	Lys	Pro	Lys	Arg
140								145						150
Gly	Asp	Thr	Tyr	Glu	Leu	Gln	Val	Arg	Gly	Phe	Ser	Ala	Glu	Gln
155								160						165
Ile	Ala	Arg	Trp	Ile	Ala	Asp	Arg	Thr	Asp	Val	Asn	Ile	Arg	Val
170								175						180
Ile	Arg	Pro	Pro	Asn	Tyr	Ala	Gly	Pro	Leu	Met	Leu	Gly	Leu	Leu
185								190						195
Leu	Ala	Val	Ile	Gly	Gly	Leu	Val	Tyr	Leu	Arg	Arg	Ser	Asn	Met
200								205						210
Glu	Phe	Leu	Phe	Asn	Lys	Thr	Gly	Trp	Ala	Phe	Ala	Ala	Leu	Cys
215								220						225
Phe	Val	Leu	Ala	Met	Thr	Ser	Gly	Gln	Met	Trp	Asn	His	Ile	Arg
230								235						240
Gly	Pro	Pro	Tyr	Ala	His	Lys	Asn	Pro	His	Thr	Gly	His	Val	Asn
245								250						255
Tyr	Ile	His	Gly	Ser	Ser	Gln	Ala	Gln	Phe	Val	Ala	Glu	Thr	His
260								265						270
Ile	Val	Leu	Leu	Phe	Asn	Gly	Gly	Val	Thr	Leu	Gly	Met	Val	Leu
275								280						285
Leu	Cys	Glu	Ala	Ala	Thr	Ser	Asp	Met	Asp	Ile	Gly	Lys	Arg	Lys
290								295						300
Ile	Met	Cys	Val	Ala	Gly	Ile	Gly	Leu	Val	Val	Leu	Phe	Phe	Ser
305								310						315
Trp	Met	Leu	Ser	Ile	Phe	Arg	Ser	Lys	Tyr	His	Gly	Tyr	Pro	Tyr
320								325						330
Ser	Phe	Leu	Met	Ser										
				335										

<210> 131

<211> 2476

<212> DNA

<213> Homo sapiens

<400> 131

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cttggcgctg gcggtactgg ccccccggagc aggggagcag aggcggagag 200
cagccaaagc gcccaatgtg gtgctggtcg tgagcgactc ctgcgtatgga 250
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ttaacagaat ctggaaataa ttttaagggt ctagatccaa attatacaac 450
atggatggat gtcatggaga ggcattggcta ccgaacacag aaattttggga 500
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tggacaagag atgttgcctt cttactcaga caagaaggca ggcccatggt 600
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tgtgaatgcc tccacccatac tgcttcgaac taaccactgg aaatatata 1400
cctattcggta tggtgcatca atattgcctc aactcttgc tcttcctcg 1450
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ttctttggat cagaagcttc attccattat aaactaccct aaagttctg 1550

cttctgtcca ccagtataat aaagagcagt ttatcaagtg gaaacaaagt 1600
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acctgtatc ccaggactt gggaggctga ggaaagcaga tcacaaggc 1900
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tatTTTgtaa gaatgttagt tatttaaga taaaatgcca atgattataa 2200
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aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa 2450
aaaaaaaaaaa aaaaaaaaaaa aaaaaaa 2476

<210> 132

<211> 536

<212> PRT

<213> Homo sapiens

<400> 132

Met	Leu	Leu	Leu	Trp	Val	Ser	Val	Val	Ala	Ala	Leu	Ala	Leu	Ala
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Val	Leu	Ala	Pro	Gly	Ala	Gly	Glu	Gln	Arg	Arg	Arg	Ala	Ala	Lys
				20				25						30

Ala	Pro	Asn	Val	Val	Leu	Val	Val	Ser	Asp	Ser	Phe	Asp	Gly	Arg
								35		40				45

Leu	Thr	Phé	His	Pro	Gly	Ser	Gln	Val	Val	Lys	Leu	Pro	Phe	Ile
								50		55				60

Asn	Phe	Met	Lys	Thr	Arg	Gly	Thr	Ser	Phe	Leu	Asn	Ala	Tyr	Thr
								65		70				75

Asn	Ser	Pro	Ile	Cys	Cys	Pro	Ser	Arg	Ala	Ala	Met	Trp	Ser	Gly
			80					85					90	
Leu	Phe	Thr	His	Leu	Thr	Glu	Ser	Trp	Asn	Asn	Phe	Lys	Gly	Leu
			95			100			100			105		
Asp	Pro	Asn	Tyr	Thr	Thr	Trp	Met	Asp	Val	Met	Glu	Arg	His	Gly
			110			115			115			120		
Tyr	Arg	Thr	Gln	Lys	Phe	Gly	Lys	Leu	Asp	Tyr	Thr	Ser	Gly	His
			125			130			130			135		
His	Ser	Ile	Ser	Asn	Arg	Val	Glu	Ala	Trp	Thr	Arg	Asp	Val	Ala
			140			145			145			150		
Phe	Leu	Leu	Arg	Gln	Glu	Gly	Arg	Pro	Met	Val	Asn	Leu	Ile	Arg
			155			160			160			165		
Asn	Arg	Thr	Lys	Val	Arg	Val	Met	Glu	Arg	Asp	Trp	Gln	Asn	Thr
			170			175			175			180		
Asp	Lys	Ala	Val	Asn	Trp	Leu	Arg	Lys	Glu	Ala	Ile	Asn	Tyr	Thr
			185			190			190			195		
Glu	Pro	Phe	Val	Ile	Tyr	Leu	Gly	Leu	Asn	Leu	Pro	His	Pro	Tyr
			200			205			205			210		
Pro	Ser	Pro	Ser	Ser	Gly	Glu	Asn	Phe	Gly	Ser	Ser	Thr	Phe	His
			215			220			220			225		
Thr	Ser	Leu	Tyr	Trp	Leu	Glu	Lys	Val	Ser	His	Asp	Ala	Ile	Lys
			230			235			235			240		
Ile	Pro	Lys	Trp	Ser	Pro	Leu	Ser	Glu	Met	His	Pro	Val	Asp	Tyr
			245			250			250			255		
Tyr	Ser	Ser	Tyr	Thr	Lys	Asn	Cys	Thr	Gly	Arg	Phe	Thr	Lys	Lys
			260			265			265			270		
Glu	Ile	Lys	Asn	Ile	Arg	Ala	Phe	Tyr	Tyr	Ala	Met	Cys	Ala	Glu
			275			280			280	"		285		
Thr	Asp	Ala	Met	Leu	Gly	Glu	Ile	Ile	Leu	Ala	Leu	His	Gln	Leu
			290			295			295			300		
Asp	Leu	Leu	Gln	Lys	Thr	Ile	Val	Ile	Tyr	Ser	Ser	Asp	His	Gly
			305			310			310			315		
Glu	Leu	Ala	Met	Glu	His	Arg	Gln	Phe	Tyr	Lys	Met	Ser	Met	Tyr
			320			325			325			330		
Glu	Ala	Ser	Ala	His	Val	Pro	Leu	Leu	Met	Met	Gly	Pro	Gly	Ile
			335			340			340			345		
Lys	Ala	Gly	Leu	Gln	Val	Ser	Asn	Val	Val	Ser	Leu	Val	Asp	Ile
			350			355			355			360		
Tyr	Pro	Thr	Met	Leu	Asp	Ile	Ala	Gly	Ile	Pro	Leu	Pro	Gln	Asn

365	370	375
Leu Ser Gly Tyr Ser Leu Leu Pro Leu Ser Ser Glu Thr Phe Lys 380	385	390
Asn Glu His Lys Val Lys Asn Leu His Pro Pro Trp Ile Leu Ser 395	400	405
Glu Phe His Gly Cys Asn Val Asn Ala Ser Thr Tyr Met Leu Arg 410	415	420
Thr Asn His Trp Lys Tyr Ile Ala Tyr Ser Asp Gly Ala Ser Ile 425	430	435
Leu Pro Gln Leu Phe Asp Leu Ser Ser Asp Pro Asp Glu Leu Thr 440	445	450
Asn Val Ala Val Lys Phe Pro Glu Ile Thr Tyr Ser Leu Asp Gln 455	460	465
Lys Leu His Ser Ile Ile Asn Tyr Pro Lys Val Ser Ala Ser Val 470	475	480
His Gln Tyr Asn Lys Glu Gln Phe Ile Lys Trp Lys Gln Ser Ile 485	490	495
Gly Gln Asn Tyr Ser Asn Val Ile Ala Asn Leu Arg Trp His Gln 500	505	510
Asp Trp Gln Lys Glu Pro Arg Lys Tyr Glu Asn Ala Ile Asp Gln 515	520	525
Trp Leu Lys Thr His Met Asn Pro Arg Ala Val 530	535	

<210> 133
<211> 1475
<212> DNA
<213> Homo sapiens

<400> 133
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gcttctactg agaggtctgc catggcctct cttggcctcc aacttgtggg 150
ctacatccta ggccttctgg ggctttggg cacactggtt gccatgctgc 200
tccccagctg gaaaacaagt tcttatgtcg gtgccagcat tgtgacagca 250
gttggcttct ccaagggcct ctggatggaa tgtgccacac acagcacagg 300
catcaccacag tgtgacatct atagcacacct tctggcctg cccgctgaca 350
tccaggctgc ccagggcatg atggtgacat ccagtgcaat ctcccccctg 400
gcctgcatta tctctgtggt gggcatgaga tgcacagtct tctgccagga 450

atccccgagcc aaagacagag tggcggtgc aggtggagtc ttttcatcc 500
ttggaggcct cctgggattc attcctgttgc cctggaatct tcataggatc 550
ctacgggact tctactcacc actgggtgcct gacagcatga aatttgagat 600
tggagaggct cttaacttgg gcattatttc ttccctgttc tccctgatag 650
ctggaatcat cctctgcttt tcctgctcat cccagagaaa tcgctccaac 700
tactacgatg cctaccaagc ccaaccttgc gccacaagga gctctccaag 750
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cagggtatgt gtgaagaacc agggggccaga gctgggggtt ggctgggtct 850
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actggatcgt gtcagaaggt gctgctgagg atagactgac tttggccatt 950
ggattgagca aaggcagaaa tggggctag tgtaacagca tgcaggttga 1000
attgccaagg atgctcgcca tgccagcctt tctgtttcc tcaccccttgc 1050
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agccaggact cagaggatcc ctttgccctc tggtttacct gggactccat 1150
ccccaaaccc actaatcaca tcccactgac tgaccctctg tgatcaaaga 1200
ccctctctct ggctgaggtt ggctcttagc tcattgctgg ggatggaaag 1250
gagaagcagt ggcttttgtg ggcattgctc taacctactt ctcaagcttc 1300
cctccaaaga aactgattgg ccctggaacc tccatcccac tcttgttatg 1350
actccacagt gtccagacta atttgtgcat gaactgaaat aaaaccatcc 1400
tacggtatcc agggAACAGA aagcaggatg caggatgggaa ggacaggaag 1450
gcagcctggg acattaaaaa aaata 1475

<210> 134

<211> 230

<212> PRT

<213> Homo sapiens

<400> 134

Met	Ala	Ser	Leu	Gly	Leu	Gln	Leu	Val	Gly	Tyr	Ile	Leu	Gly	Leu
1														15

Leu	Gly	Leu	Leu	Gly	Thr	Leu	Val	Ala	Met	Leu	Leu	Pro	Ser	Trp
														30
20									25					

Lys	Thr	Ser	Ser	Tyr	Val	Gly	Ala	Ser	Ile	Val	Thr	Ala	Val	Gly
														45
35									40					

Phe Ser Lys Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly

50	55	60
Ile Thr Gln Cys Asp Ile Tyr Ser Thr Leu Leu Gly Leu Pro Ala		
65	70	75
Asp Ile Gln Ala Ala Gln Ala Met Met Val Thr Ser Ser Ala Ile		
80	85	90
Ser Ser Leu Ala Cys Ile Ile Ser Val Val Gly Met Arg Cys Thr		
95	100	105
Val Phe Cys Gln Glu Ser Arg Ala Lys Asp Arg Val Ala Val Ala		
110	115	120
Gly Gly Val Phe Phe Ile Leu Gly Gly Leu Leu Gly Phe Ile Pro		
125	130	135
Val Ala Trp Asn Leu His Gly Ile Leu Arg Asp Phe Tyr Ser Pro		
140	145	150
Leu Val Pro Asp Ser Met Lys Phe Glu Ile Gly Glu Ala Leu Tyr		
155	160	165
Leu Gly Ile Ile Ser Ser Leu Phe Ser Leu Ile Ala Gly Ile Ile		
170	175	180
Leu Cys Phe Ser Cys Ser Ser Gln Arg Asn Arg Ser Asn Tyr Tyr		
185	190	195
Asp Ala Tyr Gln Ala Gln Pro Leu Ala Thr Arg Ser Ser Pro Arg		
200	205	210
Pro Gly Gln Pro Pro Lys Val Lys Ser Glu Phe Asn Ser Tyr Ser		
215	220	225
Leu Thr Gly Tyr Val		
230		
<210> 135		
<211> 610		
<212> DNA		
<213> Homo sapiens		
<400> 135		
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cttcgctcct gcttatgtgt cagtctgtct cctccttttg tgtccaagg 100		
aagtcatcgc tcccgtggc tcagaaccat ggctgtgcca gccggcaccc 150		
aggtgtggag acaagatcta caaccccttg gagcagtgtt gttacaatga 200		
cgccatcgtg tccctgagcg agacccgcca atgtggtccc ccctgcacct 250		
tctggccctg ctgttggactc tgctgtcttg attcctttgg cctcacaaac 300		
gattttgttg tgaagctgaa gggttcaggggt gtgaattcccc agtgccactc 350		

atctccatc tccagtaaat gtgaaagcag aagacgtttt ccctgagaag 400
acatagaaaag aaaatcaact ttcactaagg catctcagaa acataggcta 450
aggtaatatg tgtaccagta gagaagcctg aggaatttac aaaatgatgc 500
agctccaagc cattgtatgg cccatgtggg agactgatgg gacatggaga 550
atgacagtag attatcagga aataaataaa gtggttttc caatgtacac 600
acctgtaaaa 610

<210> 136

<211> 119

<212> PRT

<213> Homo sapiens

<400> 136

Met	Val	Pro	Arg	Ile	Phe	Ala	Pro	Ala	Tyr	Val	Ser	Val	Cys	Leu
1				5					10				15	

Leu	Leu	Leu	Cys	Pro	Arg	Glu	Val	Ile	Ala	Pro	Ala	Gly	Ser	Glu
			20					25				30		

Pro	Trp	Leu	Cys	Gln	Pro	Ala	Pro	Arg	Cys	Gly	Asp	Lys	Ile	Tyr
			35					40				45		

Asn	Pro	Leu	Glu	Gln	Cys	Cys	Tyr	Asn	Asp	Ala	Ile	Val	Ser	Leu
			50					55				60		

Ser	Glu	Thr	Arg	Gln	Cys	Gly	Pro	Pro	Cys	Thr	Phe	Trp	Pro	Cys
			65					70				75		

Phe	Glu	Leu	Cys	Cys	Leu	Asp	Ser	Phe	Gly	Leu	Thr	Asn	Asp	Phe
			80					85				90		

Val	Val	Lys	Leu	Lys	Val	Gln	Gly	Val	Asn	Ser	Gln	Cys	His	Ser
			95					100				105		

Ser	Pro	Ile	Ser	Ser	Lys	Cys	Glu	Ser	Arg	Arg	Arg	Phe	Pro
				110				115					

<210> 137

<211> 771

<212> DNA

<213> Homo sapiens

<400> 137

ctccactgca accacccaga gccatggctc cccgaggctg catcgtagct 50
gtctttgcca ttttctgcat ctccaggctc ctctgctcac acggagcccc 100
agtggccccc atgactcctt acctgatgct gtgccagcca cacaagagat 150
gtggggacaa gttctacgac cccctgcagc actgttgcta tgatgatgcc 200
gtcgtgcctt tggccaggac ccagacgtgt ggaaactgca ctttcagagt 250

ctgcttgag cagtgcgtcc cctggacccat catggtaag ctgataaacc 300
agaactgcga ctcagccccgg acctcgatg acaggcttg tcgcagtg 350
agctaattgga acatcagggg aacgatgact cctggattct cttccctggg 400
tgggcctgga gaaagaggct ggtgttacct gagatctggg atgctgagtg 450
gctgtttggg ggcagagaa acacacactc aactgcccac ttcattctgt 500
gacctgtctg aggcccaccc tgcaagctgcc ctgaggaggc ccacagggtcc 550
ccttctagaa ttctggacag catgagatgc gtgtgctgat gggggccca 600
ggactctgaa ccctcctgat gaccctatg gccaacatca acccggcacc 650
accccaaggc tggctggga acccttcacc cttctgtgag attttccatc 700
atctcaagtt ctcttctatc caggagcaaa gcacaggatc ataataaatt 750
tatgtacttt ataaatgaaa a 771

<210> 138

<211> 110

<212> PRT

<213> Homo sapiens.

<400> 138

Met	Ala	Pro	Arg	Gly	Cys	Ile	Val	Ala	Val	Phe	Ala	Ile	Phe	Cys
1					5				10					15

Ile	Ser	Arg	Leu	Leu	Cys	Ser	His	Gly	Ala	Pro	Val	Ala	Pro	Met
					20				25					30

Thr	Pro	Tyr	Leu	Met	Leu	Cys	Gln	Pro	His	Lys	Arg	Cys	Gly	Asp
						35			40					45

Lys	Phe	Tyr	Asp	Pro	Leu	Gln	His	Cys	Cys	Tyr	Asp	Asp	Ala	Val
					50				55					60

Val	Pro	Leu	Ala	Arg	Thr	Gln	Thr	Cys	Gly	Asn	Cys	Thr	Phe	Arg
					65				70					75

Val	Cys	Phe	Glu	Gln	Cys	Cys	Pro	Trp	Thr	Phe	Met	Val	Lys	Leu
					80				85					90

Ile	Asn	Gln	Asn	Cys	Asp	Ser	Ala	Arg	Thr	Ser	Asp	Asp	Arg	Leu
				95					100					105

Cys	Arg	Ser	Val	Ser										
				110										

<210> 139

<211> 2044

<212> DNA

<213> Homo sapiens

<400> 139

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gctcgactc agtcgcggga ggctcccg cgccggccgc gtcccgcccc 100
ctccccggca ccagaagttc ctctgcgcgt ccgacggcga catgggcgtc 150
cccacggccc tggaggccgg cagctggcgc tggggatccc tgctcttcgc 200
tctcttcctg gctgcgtccc taggtccgggt ggcagccttc aaggtcgcca 250
cgccgtattc cctgtatgtc tgtcccgagg ggcagaacgt caccctcacc 300
tgcaaggctct tggccctgt ggacaaaggg cacgatgtga ccttctacaa 350
gacgtggta cgcagctcga gggcgaggt gcagacctgc tcagagcgcc 400
ggcccatccg caaccctcacf ttccaggacc ttcacctgca ccatggaggc 450
caccaggctg ccaacaccag ccacgacctg gctcagcgcc acgggctgga 500
gtcggcctcc gaccaccatg gcaacttctc catcaccatg cgcaacctga 550
ccctgctgga tagcggcctc tactgctgcc tggtgtgga gatcaggcac 600
caccactcgg agcacaggggt ccatggtgcc atggagctgc aggtgcagac 650
aggcaaagat gcaccatcca actgtgtggt gtacccatcc tcctcccagg 700
atagtgaaaa catcacggct gcagccctgg ctacgggtgc ctgcacatcgta 750
ggaatccctct gcctccccct catcctgctc ctggcttaca agcaaaggca 800
ggcagcctcc aaccgcgtg cccaggagct ggtgcggatg gacagcaaca 850
ttcaaggat tgaaaacccc ggcttgaag cctcaccacc tgcccagggg 900
atacccgagg ccaaagtca gCACCCCTG tcctatgtgg cccagcgca 950
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tttgtggctgg gtctggggca ggtgcatttgc agccagggt ggctctgtga 1150
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gatactgtga catcccagaa gcccagcccc tcaaccctc tggatgtac 1250
atggggatgc tggacggctc agccctgtt ccaaggattt tgggtgtctg 1300
agattctccc ctagagaccc taaattcacc agctacagat gccaatgac 1350
ttacatctta agaagtctca gaacgtccag cccttcagca gctctcggtc 1400
tgagacatga gccttggat gtggcagcat cagtgggaca agatggacac 1450

tgggccaccc tcccaggcac cagacacagg gcacggtgga gagacttctc 1500
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gttgccccac ccactggaga tggtgctgag ggaggtgggt ggggccttct 1850
gggaagggtga gtggagaggg gcacctgccc cccgcctcc ccatccctca 1900
ctcccaactgc tcagcgcggg ccattgcaag ggtgccacac aatgtcttgt 1950
ccaccctggg acacttctga gtatgaagcg ggatgtctatt aaaaactaca 2000
tggggaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaga 2044

<210> 140

<211> 311

<212> PRT

<213> Homo sapiens

<400> 140

Met Gly Val Pro Thr Ala Leu Glu Ala Gly Ser Trp Arg Trp Gly
1 5 10 15

Ser Leu Leu Phe Ala Leu Phe Leu Ala Ala Ser Leu Gly Pro Val
20 25 30

Ala Ala Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro
35 40 45

Glu Gly Gln Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val
50 55 .. 60

Asp Lys Gly His Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser
65 70 75

Ser Arg Gly Glu Val Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg
80 85 90

Asn Leu Thr Phe Gln Asp Leu His Leu His His Gly Gly His Gln
95 100 105

Ala Ala Asn Thr Ser His Asp Leu Ala Gln Arg His Gly Leu Glu
110 115 120

Ser Ala Ser Asp His His Gly Asn Phe Ser Ile Thr Met Arg Asn
125 130 135

Leu Thr Leu Leu Asp Ser Gly Leu Tyr Cys Cys Leu Val Val Glu

140	145	150
Ile Arg His His His Ser Glu His Arg Val His Gly Ala Met Glu		
155	160	165
Leu Gln Val Gln Thr Gly Lys Asp Ala Pro Ser Asn Cys Val Val		
170	175	180
Tyr Pro Ser Ser Ser Gln Asp Ser Glu Asn Ile Thr Ala Ala Ala		
185	190	195
Leu Ala Thr Gly Ala Cys Ile Val Gly Ile Leu Cys Leu Pro Leu		
200	205	210
Ile Leu Leu Leu Val Tyr Lys Gln Arg Gln Ala Ala Ser Asn Arg		
215	220	225
Arg Ala Gln Glu Leu Val Arg Met Asp Ser Asn Ile Gln Gly Ile		
230	235	240
Glu Asn Pro Gly Phe Glu Ala Ser Pro Pro Ala Gln Gly Ile Pro		
245	250	255
Glu Ala Lys Val Arg His Pro Leu Ser Tyr Val Ala Gln Arg Gln		
260	265	270
Pro Ser Glu Ser Gly Arg His Leu Leu Ser Glu Pro Ser Thr Pro		
275	280	285
Leu Ser Pro Pro Gly Pro Gly Asp Val Phe Phe Pro Ser Leu Asp		
290	295	300
Pro Val Pro Asp Ser Pro Asn Phe Glu Val Ile		
305	310	

<210> 141
 <211> 1732
 <212> DNA
 <213> Homo sapiens

<400> 141
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 ctttagacctc ctttcctgcc ctcccttc gcccaccgct gttcctggc 150
 ctttctccga ccccgctcta gcagcagacc tcctgggtc tgtgggtta 200
 tctgtggccc ctgtgcctcc gtgtcctttt cgtctccctt cttcccgact 250
 ccgctcccg accagcggcc tgaccctgg gaaaggatgg ttcccgaggt 300
 gagggtcctc tcctccttgc tggactcgc gctgctctgg ttccccctgg 350
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 agataactccc ccggcgagag ctggcacccc tacttgagc cacaaggcct 450

gatgtactgc ctgcgctgta cctgctcaga gggcgcccat gtgagttgtt 500
accgcctcca ctgtccgcct gtccactgcc cccagcctgt gacggagcca 550
cagcaatgtc gtcccaagtgc tggaaacct cacactccct ctggactccg 600
ggccccacca aagtccgtcc agcacaacgg gaccatgtac caacacggag 650
agatcttcag tgcccatgag ctgttccct cccgcctgcc caaccagtgt 700
gtcctctgca gctgcacaga gggccagatc tactgcggcc tcacaacctg 750
ccccgaacca ggctgcccag caccctccc actgccagac tcctgctgcc 800
aagcctgcaa agatgaggca agtgagcaat cgatgaaaga ggacagtgtg 850
cagtcgtcc atgggttag acatcctcag gatccatgtt ccagtgtatgc 900
tgggagaaaag agaggccccgg gcaccccaagc ccccaactggc ctcagcgccc 950
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actgtcaaga tcgtccctgaa ggagaaacat aagaaagcct gtgtgcattgg 1050
cgaaaaagacg tactcccacg gggaggtgtg gcacccggcc ttccgtgcct 1100
tcggcccccctt gccctgcatac ctatgcacccgtt gtgaggatgg ccggcaggac 1150
tgccagcgtg tgacctgtcc caccgagttac ccctgcccgtc accccgagaa 1200
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gccacagtga gatcagttct accaggtgtc ccaaggcacc gggccgggtc 1300
ctcgccaca catcggtatc cccaaagccca gacaacctgc gtcgtttgc 1350
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gaaggtcact ggaacgtctt cctagcccaag accctggagc tgaaggtcac 1600
ggccagtcac gacaaagtga ccaagacata acaaagacct aacagttgca 1650
gatatgagct gtataattgt tggttattata tattaataaa taagaagttg 1700
cattaccctc aaaaaaaaaa aaaaaaaaaa aa 1732

<210> 142
<211> 451

<212> PRT

<213> Homo sapiens

<400> 142

Met Val Pro Glu Val Arg Val Leu Ser Ser Leu Leu Gly Leu Ala
 1 5 10 15

Leu Leu Trp Phe Pro Leu Asp Ser His Ala Arg Ala Arg Pro Asp
 20 25 30

Met Phe Cys Leu Phe His Gly Lys Arg Tyr Ser Pro Gly Glu Ser
 35 40 45

Trp His Pro Tyr Leu Glu Pro Gln Gly Leu Met Tyr Cys Leu Arg
 50 55 60

Cys Thr Cys Ser Glu Gly Ala His Val Ser Cys Tyr Arg Leu His
 65 70 75

Cys Pro Pro Val His Cys Pro Gln Pro Val Thr Glu Pro Gln Gln
 80 85 90

Cys Cys Pro Lys Cys Val Glu Pro His Thr Pro Ser Gly Leu Arg
 95 100 105

Ala Pro Pro Lys Ser Cys Gln His Asn Gly Thr Met Tyr Gln His
 110 115 120

Gly Glu Ile Phe Ser Ala His Glu Leu Phe Pro Ser Arg Leu Pro
 125 130 135

Asn Gln Cys Val Leu Cys Ser Cys Thr Glu Gly Gln Ile Tyr Cys
 140 145 150

Gly Leu Thr Thr Cys Pro Glu Pro Gly Cys Pro Ala Pro Leu Pro
 155 160 165

Leu Pro Asp Ser Cys Cys Gln Ala Cys Lys Asp Glu Ala Ser Glu
 170 175 180

Gln Ser Asp Glu Glu Asp Ser Val Gln Ser Leu His Gly Val Arg
 185 190 195

His Pro Gln Asp Pro Cys Ser Ser Asp Ala Gly Arg Lys Arg Gly
 200 205 210

Pro Gly Thr Pro Ala Pro Thr Gly Leu Ser Ala Pro Leu Ser Phe
 215 220 225

Ile Pro Arg His Phe Arg Pro Lys Gly Ala Gly Ser Thr Thr Val
 230 235 240

Lys Ile Val Leu Lys Glu Lys His Lys Lys Ala Cys Val His Gly
 245 250 255

Gly Lys Thr Tyr Ser His Gly Glu Val Trp His Pro Ala Phe Arg
 260 265 270

Ala Phe Gly Pro Leu Pro Cys Ile Leu Cys Thr Cys Glu Asp Gly
 275 280 285

Arg Gln Asp Cys Gln Arg Val Thr Cys Pro Thr Glu Tyr Pro Cys

290	295	300
Arg His Pro Glu Lys Val Ala Gly Lys Cys Cys Lys Ile Cys Pro		
305	310	315
Glu Asp Lys Ala Asp Pro Gly His Ser Glu Ile Ser Ser Thr Arg		
320	325	330
Cys Pro Lys Ala Pro Gly Arg Val Leu Val His Thr Ser Val Ser		
335	340	345
Pro Ser Pro Asp Asn Leu Arg Arg Phe Ala Leu Glu His Glu Ala		
350	355	360
Ser Asp Leu Val Glu Ile Tyr Leu Trp Lys Leu Val Lys Asp Glu		
365	370	375
Glu Thr Glu Ala Gln Arg Gly Glu Val Pro Gly Pro Arg Pro His		
380	385	390
Ser Gln Asn Leu Pro Leu Asp Ser Asp Gln Glu Ser Gln Glu Ala		
395	400	405
Arg Leu Pro Glu Arg Gly Thr Ala Leu Pro Thr Ala Arg Trp Pro		
410	415	420
Pro Arg Arg Ser Leu Glu Arg Leu Pro Ser Pro Asp Pro Gly Ala		
425	430	435
Glu Gly His Gly Gln Ser Arg Gln Ser Asp Gln Asp Ile Thr Lys		
440	445	450

Thr

<210> 143
<211> 693
<212> DNA
<213> Homo sapiens

<400> 143
ctagcctgcg ccaagggtta gtgagaccgc gcggcaacag cttgcggctg 50
cggggagctc ccgtggcgcc tccgctggct gtgcaggcgg ccatggattc 100
cttgcggaaa atgctgatct cagtcgcaat gctggcgca ggggctggcg 150
tgggctacgc gtcctcggtt atcgtgaccc cgggagagcgc gcggaaagcag 200
gaaatgctaa aggagatgcc actgcaggac ccaaggagca gggaggaggc 250
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aactgaaga accaataaaa tcatgttcct ccaaaaaaaaaaaaaaaa 650
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 693

<210> 144

<211> 93

<212> PRT

<213> Homo sapiens

<400> 144

Met	Asp	Ser	Leu	Arg	Lys	Met	Leu	Ile	Ser	Val	Ala	Met	Leu	Gly
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Ala	Gly	Ala	Gly	Val	Gly	Tyr	Ala	Leu	Leu	Val	Ile	Val	Thr	Pro
				20					25				30	

Gly	Glu	Arg	Arg	Lys	Gln	Glu	Met	Leu	Lys	Glu	Met	Pro	Leu	Gln
				35					40				45	

Asp	Pro	Arg	Ser	Arg	Glu	Glu	Ala	Ala	Arg	Thr	Gln	Gln	Leu	Leu
					50				55				60	

Leu	Ala	Thr	Leu	Gln	Glu	Ala	Ala	Thr	Thr	Gln	Glu	Asn	Val	Ala
				65					70				75	

Trp	Arg	Lys	Asn	Trp	Met	Val	Gly	Gly	Glu	Gly	Gly	Ala	Ser	Gly
					80				85				90	

Arg Ser Pro

<210> 145

<211> 1883

<212> DNA

<213> Homo sapiens

<400> 145

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atggtcggga cccctccaag gacagcagca ccacccgtg gatgtatgg 200

aacgccgact agctgctta gaggaacggc tggcccgatg ccaggaccag 250

agttagtcggc atgctgctga gctgcgggac ttcaagaaca agatgctgcc 300

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acaccatctc cgggagagtg gatcgcttgg agcgggaggt agactatctg 400

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tggaggccct gggaccaaag gcaagggaag aaggaatgag aagtacgata 500
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aaaaatccac aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1850

aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaa 1883

<210> 146

<211> 406

<212> PRT

<213> Homo sapiens

<400> 146

Met Gly Pro Ser Thr Pro Leu Leu Ile Leu Phe Leu Leu Ser Trp
1 5 10 15

Ser Gly Pro Leu Gln Gly Gln His His Leu Val Glu Tyr Met
20 25 30

Glu Arg Arg Leu Ala Ala Leu Glu Glu Arg Leu Ala Gln Cys Gln
35 40 45

Asp Gln Ser Ser Arg His Ala Ala Glu Leu Arg Asp Phe Lys Asn
50 55 60

Lys Met Leu Pro Leu Leu Glu Val Ala Glu Lys Glu Arg Glu Ala
65 70 75

Leu Arg Thr Glu Ala Asp Thr Ile Ser Gly Arg Val Asp Arg Leu
80 85 90

Glu Arg Glu Val Asp Tyr Leu Glu Thr Gln Asn Pro Ala Leu Pro
95 100 105

Cys Val Glu Phe Asp Glu Lys Val Thr Gly Gly Pro Gly Thr Lys
110 115 120

Gly Lys Gly Arg Arg Asn Glu Lys Tyr Asp Met Val Thr Asp Cys
125 130 135

Gly Tyr Thr Ile Ser Gln Val Arg Ser Met Lys Ile Leu Lys Arg
140 145 150

Phe Gly Gly Pro Ala Gly Leu Trp Thr Lys Asp Pro Leu Gly Gln
155 160 165

Thr Glu Lys Ile Tyr Val Leu Asp Gly Thr Gln Asn Asp Thr Ala
170 175 180

Phe Val Phe Pro Arg Leu Arg Asp Phe Thr Leu Ala Met Ala Ala
185 190 195

Arg Lys Ala Ser Arg Val Arg Val Pro Phe Pro Trp Val Gly Thr
200 205 210

Gly Gln Leu Val Tyr Gly Gly Phe Leu Tyr Phe Ala Arg Arg Pro
215 220 225

Pro Gly Arg Pro Gly Gly Gly Glu Met Glu Asn Thr Leu Gln
230 235 240

Leu Ile Lys Phe His Leu Ala Asn Arg Thr Val Val Asp Ser Ser
245 250 255

Val Phe Pro Ala Glu Gly Leu Ile Pro Pro Tyr Gly Leu Thr Ala
 260 265 270
 Asp Thr Tyr Ile Asp Leu Val Ala Asp Glu Glu Gly Leu Trp Ala
 275 280 285
 Val Tyr Ala Thr Arg Glu Asp Asp Arg His Leu Cys Leu Ala Lys
 290 295 300
 Leu Asp Pro Gln Thr Leu Asp Thr Glu Gln Gln Trp Asp Thr Pro
 305 310 315
 Cys Pro Arg Glu Asn Ala Glu Ala Ala Phe Val Ile Cys Gly Thr
 320 325 330
 Leu Tyr Val Val Tyr Asn Thr Arg Pro Ala Ser Arg Ala Arg Ile
 335 340 345
 Gln Cys Ser Phe Asp Ala Ser Gly Thr Leu Thr Pro Glu Arg Ala
 350 355 360
 Ala Leu Pro Tyr Phe Pro Arg Arg Tyr Gly Ala His Ala Ser Leu
 365 370 375
 Arg Tyr Asn Pro Arg Glu Arg Gln Leu Tyr Ala Trp Asp Asp Gly
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 Tyr Gln Ile Val Tyr Lys Leu Glu Met Arg Lys Lys Glu Glu Glu
 395 400 405
 Val

<210> 147
 <211> 2052
 <212> DNA
 <213> Homo sapiens

<400> 147
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 gttctccctct tctctcta at ccatccgtca cctccctgt catccgtttc 150
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 ttggttctga gtctcctcaa gctgggatca gggcagtggc aggtgtttgg 250
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 agggggccagt tctctagcgt ggtccacactc tacagggacg ggaaggacca 400
 gccatttatg cagatgccac agtatcaagg caggacaaaa ctggtaagg 450
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tttccatcac gggatatgtt gatagagaca tccagctact ctgtcagtc 650
tcgggcttgt tccccggcc cacagcgaag tggaaaggc cacaaggaca 700
ggatttgccc acagactcca ggacaaacag agacatgcat ggcctgttg 750
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tccatgoggc atgctcatct gagccgagag gtgaaatcca gggtacagat 850
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ccacctctca ggtgaagaac cgtaggaat tccatctca caggctgtgg 1950

tgtagattaa gtagacaagg aatgtgaata atgcttagat cttattgatg 2000
 acagagtcta tcctaatggc ttgttcatta tattacactt tcagtaaaaa 2050
 aa 2052
 <210> 148
 <211> 500
 <212> PRT
 <213> Homo sapiens
 <400> 148
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 Ser Gly Gln Trp Gln Val Phe Gly Pro Asp Lys Pro Val Gln Ala
 20 25 30
 Leu Val Gly Glu Asp Ala Ala Phe Ser Cys Phe Leu Ser Pro Lys
 35 40 45
 Thr Asn Ala Glu Ala Met Glu Val Arg Phe Phe Arg Gly Gln Phe
 50 55 60
 Ser Ser Val Val His Leu Tyr Arg Asp Gly Lys Asp Gln Pro Phe
 65 70 75
 Met Gln Met Pro Gln Tyr Gln Gly Arg Thr Lys Leu Val Lys Asp
 80 85 90
 Ser Ile Ala Glu Gly Arg Ile Ser Leu Arg Leu Glu Asn Ile Thr
 95 100 105
 Val Leu Asp Ala Gly Leu Tyr Gly Cys Arg Ile Ser Ser Gln Ser
 110 115 120
 Tyr Tyr Gln Lys Ala Ile Trp Glu Leu Gln Val Ser Ala Leu Gly
 125 130 135
 Ser Val Pro Leu Ile Ser Ile Thr Gly Tyr Val Asp Arg Asp Ile
 140 145 150
 Gln Leu Leu Cys Gln Ser Ser Gly Trp Phe Pro Arg Pro Thr Ala
 155 160 165
 Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Thr Asp Ser Arg
 170 175 180
 Thr Asn Arg Asp Met His Gly Leu Phe Asp Val Glu Ile Ser Leu
 185 190 195
 Thr Val Gln Glu Asn Ala Gly Ser Ile Ser Cys Ser Met Arg His
 200 205 210
 Ala His Leu Ser Arg Glu Val Glu Ser Arg Val Gln Ile Gly Asp
 215 220 225
 Thr Phe Phe Glu Pro Ile Ser Trp His Leu Ala Thr Lys Val Leu

230	235	240
Gly Ile Leu Cys Cys Gly Leu Phe Phe	Gly Ile Val Gly Leu Lys	
245	250	255
Ile Phe Phe Ser Lys Phe Gln Trp Lys	Ile Gln Ala Glu Leu Asp	
260	265	270
Trp Arg Arg Lys His Gly Gln Ala Glu	Leu Arg Asp Ala Arg	Lys
275	280	285
His Ala Val Glu Val Thr Leu Asp Pro	Glu Thr Ala His Pro	Lys
290	295	300
Leu Cys Val Ser Asp Leu Lys Thr Val	Thr His Arg Lys Ala	Pro
305	310	315
Gln Glu Val Pro His Ser Glu Lys Arg	Phe Thr Arg Lys Ser	Val
320	325	330
Val Ala Ser Gln Ser Phe Gln Ala Gly	Lys His Tyr Trp Glu	Val
335	340	345
Asp Gly Gly His Asn Lys Arg Trp Arg	Val Gly Val Cys Arg	Asp
350	355	360
Asp Val Asp Arg Arg Lys Glu Tyr Val	Thr Leu Ser Pro Asp	His
365	370	375
Gly Tyr Trp Val Leu Arg Leu Asn Gly	Glu His Leu Tyr Phe	Thr
380	385	390
Leu Asn Pro Arg Phe Ile Ser Val Phe	Pro Arg Thr Pro Pro	Thr
395	400	405
Lys Ile Gly Val Phe Leu Asp Tyr Glu	Cys Gly Thr Ile Ser	Phe
410	415	420
Phe Asn Ile Asn Asp Gln Ser Leu Ile	Tyr Thr Leu Thr Cys	Arg
425	430	435
Phe Glu Gly Leu Leu Arg Pro Tyr Ile	Glu Tyr Pro Ser Tyr	Asn
440	445	450
Glu Gln Asn Gly Thr Pro Ile Val Ile	Cys Pro Val Thr Gln	Glu
455	460	465
Ser Glu Lys Glu Ala Ser Trp Gln Arg	Ala Ser Ala Ile Pro	Glu
470	475	480
Thr Ser Asn Ser Glu Ser Ser Ser Gln	Ala Thr Thr Pro Phe	Leu
485	490	495
Pro Arg Gly Glu Met		
500		

<210> 149
<211> 24

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 149
gcgtggtcca cctctacagg gacg 24

<210> 150 *
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 150
ggaactgacc cagtgtgac acc 23

<210> 151
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 151
gcagatgcc a cagtatcaag gcaggacaaa actggtaag gattc 45

<210> 152
<211> 2294
<212> DNA
<213> Homo sapiens

<400> 152
gcatggtc gcccgggtggc ggtggcgccg gcgggtgcgg aggttcctt 50
ggtcggattt caacgaggag aagatgactg accaaccgac tggctaatg 100
aatgaatggc ggagccgagc ggcggatgag gagcctggcg agcctggcg 150
gcctcgccct gtttgtctgc gccggccggc cggccggcgt cgcctcagcc 200
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cgctcgccgg ggccccgggt tgccggggcga gcccagccac cccttcccta 300
ggcgacggc tccccacggcc caggccccga ggaccggcc cccgcgcgcc 350
accgtccacc gaccctggc tgcgacttct ccagccagt ccccgagac 400

caccctctt tggcgactg ctggaccctc ttccaccacc tttcaggcgc 450
cgctcgcccc ctcgccgacc acccctccgg cgccggaacg cacttcgacc 500
acctctcagg cgccgaccag acccgccgacc accaccctt cgacgaccac 550
tggcccgccg ccgaccaccc ctgttagcgac caccgtaccg gcgcccacga 600
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aagcaacaga gggtggact gaagtttatt ttattttagc aaggaaaaaa 950
aaaaggctgc tactctcaag gaccatactg gtttaaaca aggaggatga 1000
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atgttatatt taatgtcagg atttaaaac atctaattta ctgatttagt 1100
tcttcaaaag cactagagtc gccaattttt ctctggata atttctgtaa 1150
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agagggagac tctgtcttaa aaaaaaaaaa aaaaaaaaaa aaaa 2294

<210> 153

<211> 258

<212> PRT

<213> Homo sapiens

<400> 153

Met	Arg	Ser	Leu	Pro	Ser	Leu	Gly	Gly	Leu	Ala	Leu	Leu	Cys	Cys
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Ala	Ala	Ala	Ala	Ala	Ala	Val	Ala	Ser	Ala	Ala	Ser	Ala	Gly	Asn
						20			25					30
Val	Thr	Gly	Gly	Gly	Gly	Ala	Ala	Gly	Gln	Val	Asp	Ala	Ser	Pro
						35			40					45
Gly	Pro	Gly	Leu	Arg	Gly	Glu	Pro	Ser	His	Pro	Phe	Pro	Arg	Ala
						50			55					60
Thr	Ala	Pro	Thr	Ala	Gln	Ala	Pro	Arg	Thr	Gly	Pro	Pro	Arg	Ala
						65			70					75
Thr	Val	His	Arg	Pro	Leu	Ala	Ala	Thr	Ser	Pro	Ala	Gln	Ser	Pro
						80			85					90
Glu	Thr	Thr	Pro	Leu	Trp	Ala	Thr	Ala	Gly	Pro	Ser	Ser	Thr	Thr
						95			100					105
Phe	Gln	Ala	Pro	Leu	Gly	Pro	Ser	Pro	Thr	Thr	Pro	Pro	Ala	Ala
						110			115					120
Glu	Arg	Thr	Ser	Thr	Thr	Ser	Gln	Ala	Pro	Thr	Arg	Pro	Ala	Pro
														135
Thr	Thr	Leu	Ser	Thr	Thr	Thr	Gly	Pro	Ala	Pro	Thr	Thr	Pro	Val
														140
Ala	Thr	Thr	Val	Pro	Ala	Pro	Thr	Thr	Pro	Arg	Thr	Pro	Thr	Pro
														155
Asp	Leu	Pro	Ser	Ser	Ser	Asn	Ser	Ser	Val	Leu	Pro	Thr	Pro	Pro
														160

170 175 180
Ala Thr Glu Ala Pro Ser Ser Pro Pro Pro Glu Tyr Val Cys Asn
185 190 195
Cys Ser Val Val Gly Ser Leu Asn Val Asn Arg Cys Asn Gln Thr
200 205 210
Thr Gly Gln Cys Glu Cys Arg Pro Gly Tyr Gln Gly Leu His Cys
215 220 225
Glu Thr Cys Lys Glu Gly Phe Tyr Leu Asn Tyr Thr Ser Gly Leu
230 235 240
Cys Gln Pro Cys Asp Cys Ser Pro His Gly Ala Leu Ser Ile Pro
245 250 255
Cys Asn Arg

<210> 154

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 154

aactgctctg tgggttggaaag cctg 24

<210> 155

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 155

cagtacatcg gctgacagac ccac 24

<210> 156

<211> 38

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-38

<223> Synthetic construct.

<400> 156

aggttatccatg gggcttcact gtgaaacctg caaagagg 38

<210> 157
 <211> 689
 <212> DNA
 <213> Homo sapiens

<400> 157
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 ttctggcttt ggtctcggtg cccagggccc aggccgtgtg gttggaaaga 100
 ctggaccctg agcagcttct tacgtgcttgc cggtggcctc 150
 ccgggaaaag ggcttgcca tggagaagga catgaagaac gtcgtgggg 200
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 ctccggatgg gtgttgaga atccctcaat aggctgtgtg gagctctggg 350
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 gggcccaagca ccagctcaga ataaagcgat tccacagca 689

<210> 158
 <211> 163
 <212> PRT
 <213> Homo sapiens

<400> 158
 Met Gly Gly Leu Leu Leu Ala Ala Phe Leu Ala Leu Val Ser Val
 1 5 10 15
 Pro Arg Ala Gln Ala Val Trp Leu Gly Arg Leu Asp Pro Glu Gln
 20 25 30
 Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys
 35 40 45
 Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val
 50 55 60
 Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln
 65 70 75
 His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys
 80 85 90

Arg Asn Ser Gly Trp Val Phe Glu Asn Pro Ser Ile Gly Val Leu
95 100 105

Glu Leu Trp Val Leu Ala Thr Asn Phe Arg Asp Tyr Ala Ile Ile
110 115 120

Phe Thr Gln Leu Glu Phe Gly Asp Glu Pro Phe Asn Thr Val Glu
125 130 135

Leu Tyr Ser Leu Thr Glu Thr Ala Ser Gln Glu Ala Met Gly Leu
140 145 150

Phe Thr Lys Trp Ser Arg Ser Leu Gly Phe Leu Ser Gln
155 160

<210> 159
<211> 1665
<212> DNA
<213> Homo sapiens

<400> 159
aacagacgtt ccctcgccgc cctggcacct ctaacccag acatgctgct 50
gctgctgctg cccctgctct gggggaggga gagggcggaa ggacagacaa 100
gtaaaactgct gacgatgcag agttccgtga cggtgcagga aggccctgtgt 150
gtccatgtgc cctgctcctt ctcctacccc tcgcatggct ggatttaccc 200
tggcccaagta gttcatggct actgggttccg ggaaggggcc aatacagacc 250
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actcgggacc gattccacct ccttggggac ccacatacca agaattgcac 350
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gccccaggac catggcacca gcctcacctg tcaggtgacc ttccctgggg 700
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caccgagttac tcggagatca agatccacag atgagaaaact gcagagactc 1450
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tgattcttgt agaattaaca gccctcaacg tgatgagcta tgataaacact 1550
atgaattatg tgcagagtga aaagcacaca ggcttagag tcaaagtatc 1600
tcaaacctga atccacactg tgccctccct tttttttt taactaaaag 1650
acagacaaat tccta 1665

<210> 160

<211> 463

<212> PRT

<213> Homo sapiens

<400> 160

Met	Leu	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Trp	Gly	Arg	Glu	Arg	Ala
1					5				10					15

Glu	Gly	Gln	Thr	Ser	Lys	Leu	Leu	Thr	Met	Gln	Ser	Ser	Val	Thr
					20				25					30

Val	Gln	Glu	Gly	Leu	Cys	Val	His	Val	Pro	Cys	Ser	Phe	Ser	Tyr
				35				40						45

Pro	Ser	His	Gly	Trp	Ile	Tyr	Pro	Gly	Pro	Val	Val	His	Gly	Tyr
				50				55						60

Trp	Phe	Arg	Glu	Gly	Ala	Asn	Thr	Asp	Gln	Asp	Ala	Pro	Val	Ala
					65			70						75

Thr	Asn	Asn	Pro	Ala	Arg	Ala	Val	Trp	Glu	Glu	Thr	Arg	Asp	Arg
					80				85					90

Phe	His	Leu	Leu	Gly	Asp	Pro	His	Thr	Lys	Asn	Cys	Thr	Leu	Ser
					95				100					105

Ile Arg Asp Ala Arg Arg Ser Asp Ala Gly Arg Tyr Phe Arg

110	115	120
Met Glu Lys Gly Ser Ile Lys Trp Asn Tyr Lys His His Arg Leu		
125	130	135
Ser Val Asn Val Thr Ala Leu Thr His Arg Pro Asn Ile Leu Ile		
140	145	150
Pro Gly Thr Leu Glu Ser Gly Cys Pro Gln Asn Leu Thr Cys Ser		
155	160	165
Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met Ile Ser Trp		
170	175	180
Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr Arg Ser		
185	190	195
Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr Ser		
200	205	210
Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn		
215	220	225
Lys Thr Val His Leu Asn Val Ser Tyr Pro Pro Gln Asn Leu Thr		
230	235	240
Met Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly		
245	250	255
Asn Gly Ser Ser Leu Ser Leu Pro Glu Gly Gln Ser Leu Arg Leu		
260	265	270
Val Cys Ala Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu		
275	280	285
Ser Leu Ser Trp Arg Gly Leu Thr Leu Cys Pro Ser Gln Pro Ser		
290	295	300
Asn Pro Gly Val Leu Glu Leu Pro Trp Val His Leu Arg Asp Ala		
305	310	315
Ala Glu Phe Thr Cys Arg Ala Gln Asn Pro Leu Gly Ser Gln Gln		
320	325	330
Val Tyr Leu Asn Val Ser Leu Gln Ser Lys Ala Thr Ser Gly Val		
335	340	345
Thr Gln Gly Val Val Gly Gly Ala Gly Ala Thr Ala Leu Val Phe		
350	355	360
Leu Ser Phe Cys Val Ile Phe Val Val Val Arg Ser Cys Arg Lys		
365	370	375
Lys Ser Ala Arg Pro Ala Ala Gly Val Gly Asp Thr Gly Ile Glu		
380	385	390
Asp Ala Asn Ala Val Arg Gly Ser Ala Ser Gln Gly Pro Leu Thr		
395	400	405

Glu Pro Trp Ala Glu Asp Ser Pro Pro Asp Gln Pro Pro Pro Ala
410 415 420
Ser Ala Arg Ser Ser Val Gly Gly Glu Leu Gln Tyr Ala Ser
425 430 435
Leu Ser Phe Gln Met Val Lys Pro Trp Asp Ser Arg Gly Gln Glu
440 445 450
Ala Thr Asp Thr Glu Tyr Ser Glu Ile Lys Ile His Arg
455 460

<210> 161
<211> 739
<212> DNA
<213> Homo sapiens

<400> 161
gacgcccagt gacctgccga ggtcgccagc acagagctct ggagatgaag 50
accctgttcc tgggtgtcac gctcgccctg gccgctgccc tgtccttcac 100
cctggaggag gaggatatca cagggacctg gtacgtgaag gccatggtgg 150
tcgataagga ctttccggag gacaggaggc ccaggaaggt gtccccagtg 200
aaggtgacag ccctgggcgg tggaaagttg gaagccacgt tcaccttcat 250
gagggaggat cggtgcattcc agaagaaaat cctgatgcgg aagacggagg 300
agcctggcaa atacagcgcc tatggggca ggaagctcat gtacctgcag 350
gagctgcca ggagggacca ctacatctt tactgcaaag accagcacca 400
tggggccctg ctccacatgg gaaagcttgt ggtaggaat tctgatacca 450
accgggaggc cctgaaagaa tttaagaaat tggcagcg caagggactc 500
tcggaggagg acatttcac gcccctgcag acgggaagct gcgttcccg 550
acacttaggca gccccgggt ctgcacctcc agagccacc ctaccaccag 600
acacagagcc cggaccaccc ggacctaccc tccagccatg acccttcct 650
gctcccaccc acctgactcc aaataaagtc cttttcccc aaaaaaaaaa 700
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162
<211> 170
<212> PRT
<213> Homo sapiens

<400> 162
Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala
1 5 10 15
Leu Ser Phe Thr Leu Glu Glu Asp Ile Thr Gly Thr Trp Tyr

20	25	30
Val Lys Ala Met Val Val Asp Lys Asp Phe Pro Glu Asp Arg Arg		
35	40	45
Pro Arg Lys Val Ser Pro Val Lys Val Thr Ala Leu Gly Gly Gly		
50	55	60
Lys Leu Glu Ala Thr Phe Thr Phe Met Arg Glu Asp Arg Cys Ile		
65	70	75
Gln Lys Lys Ile Leu Met Arg Lys Thr Glu Glu Pro Gly Lys Tyr		
80	85	90
Ser Ala Tyr Gly Gly Arg Lys Leu Met Tyr Leu Gln Glu Leu Pro		
95	100	105
Arg Arg Asp His Tyr Ile Phe Tyr Cys Lys Asp Gln His His Gly		
110	115	120
Gly Leu Leu His Met Gly Lys Leu Val Gly Arg Asn Ser Asp Thr		
125	130	135
Asn Arg Glu Ala Leu Glu Glu Phe Lys Lys Leu Val Gln Arg Lys		
140	145	150
Gly Leu Ser Glu Glu Asp Ile Phe Thr Pro Leu Gln Thr Gly Ser		
155	160	165
Cys Val Pro Glu His		
170		

<210> 163
<211> 22
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-22
<223> Synthetic construct.

<400> 163
ggagatgaag accctgttcc tg 22

<210> 164
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-26
<223> Synthetic construct.

<400> 164
ggagatgaag accctgttcc tgggtg 26

<210> 165
<211> 21
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-21
<223> Synthetic construct.

<400> 165
gtcctccgga aagtccat c 21

<210> 166
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 166
gccttagtgtt cggaaacgca gcttc 25

<210> 167
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 167
cagggacctg gtacgtgaag gccatggtgg tcgataagga ctttccggag 50

<210> 168
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 168
ctgtcctca ccctggagga ggaggatatc acagggacct ggtac 45

<210> 169
<211> 1204
<212> DNA
<213> Homo sapiens

<400> 169

gttccgcaga tgcagagggtt gaggtggctg cgggactgga agtcatcggg 50
cagagggtctc acagcagcca aggaacctgg ggcccgctcc tccccctcc 100
aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 150
gtagggggag agaccaggat catcaagggg ttcgagtgca agcctcactc 200
ccagccctgg caggcagccc tgttcgagaa gacgcggcta ctctgtggg 250
cgacgctcat cgcccccaga tggctcctga cagcagccca ctgcctcaag 300
ccccgctaca tagttcacct ggggcagcac aacctccaga aggaggaggg 350
ctgtgagcac accccggacag ccactgagtc cttccccac cccggcttca 400
acaacagcct ccccaacaaa gaccaccgca atgacatcat gctggtgaag 450
atggcatcgc cagtctccat cacctggct gtgcgacccc tcaccctctc 500
ctcacgctgt gtcactgctg gcaccagctg cctcatttcc ggctggggca 550
gcacgtccag cccccagttt cgcctgcctc acacccttgcg atgcgccaa 600
atcaccatca ttgagcacca gaagtgttag aacgcctacc ccggcaacat 650
cacagacacc atggtgtgtg ccagcgtgca ggaagggggc aaggactcct 700
gccagggtga ctccggggc cctctggct gtaaccagtc tcttcaaggc 750
attatctcct gggccagga tccgtgtgct atcacccgaa agcctggtgt 800
ctacacgaaa gtctgcaa atgtggactg gatccaggag acgtatgaaga 850
acaatttagac tggacccacc caccacagcc catcaccctc catttccact 900
tggtgtttgg ttccctgttca ctctgttaat aagaaaccct aagccaagac 950
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taataatcaa cctggggttc gaaatcagt agacctggat tcaaattctg 1050
ccttgaataa ttgtgactct gggaatgaca acacctggtt tggctctgt 1100
tgtatccccca gccccaaaga cagctcctgg ccatatatca aggtttcaat 1150
aaatatttgc taaatgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1200
aaaa 1204

<210> 170
<211> 250
<212> PRT
<213> Homo sapiens

<400> 170
Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu
1 5 10 15

Val Gly Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro
 20 25 30
 His Ser Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu
 35 40 45
 Leu Cys Gly Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala
 50 55 60
 Ala His Cys Leu Lys Pro Arg Tyr Ile Val His Leu Gly Gln His
 65 70 75
 Asn Leu Gln Lys Glu Glu Gly Cys Glu Gln Thr Arg Thr Ala Thr
 80 85 90
 Glu Ser Phe Pro His Pro Gly Phe Asn Asn Ser Leu Pro Asn Lys
 95 100 105
 Asp His Arg Asn Asp Ile Met Leu Val Lys Met Ala Ser Pro Val
 110 115 120
 Ser Ile Thr Trp Ala Val Arg Pro Leu Thr Leu Ser Ser Arg Cys
 125 130 135
 Val Thr Ala Gly Thr Ser Cys Leu Ile Ser Gly Trp Gly Ser Thr
 140 145 150
 Ser Ser Pro Gln Leu Arg Leu Pro His Thr Leu Arg Cys Ala Asn
 155 160 165
 Ile Thr Ile Ile Glu His Gln Lys Cys Glu Asn Ala Tyr Pro Gly
 170 175 180
 Asn Ile Thr Asp Thr Met Val Cys Ala Ser Val Gln Glu Gly Gly
 185 190 195
 Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Asn
 200 205 210
 Gln Ser Leu Gln Gly Ile Ile Ser Trp Gly Gln Asp Pro Cys Ala
 215 220 225
 Ile Thr Arg Lys Pro Gly Val Tyr Thr Lys Val Cys Lys Tyr Val
 230 235 240
 Asp Trp Ile Gln Glu Thr Met Lys Asn Asn
 245 250
 <210> 171
 <211> 25
 <212> DNA
 <213> Artificial
 <220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 171
ggctgcggga ctgaaagtca tcggg 25

<210> 172
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 172
ctccaggcca tgaggattct gcag 24

<210> 173
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 173
cctctggtct gtaaccag 18

<210> 174
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 174
tctgtatgt tgccgggta ggcg 24

<210> 175
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 175
cgttagaca ccaggtttc gggtg 25

<210> 176
<211> 18
<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-18

<223> Synthetic construct.

<400> 176
cccttgatga tcctggtc 18

<210> 177

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 177
aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 50

<210> 178

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 178
gagagaccag gatcatcaag gggttcgagt gcaaggctca ctc 43

<210> 179

<211> 907

<212> DNA

<213> Homo sapiens

<400> 179
gagcagtgtt ctgctggagc cgatgccaaa aaccatgcat ttcttattca 50
gattcattgt ttttttat ctgtggggcc tttttactgc tcagagacaa 100
aagaaaagagg agagcaccga agaagtgaaa atagaagttt tgcatcgccc 150
agaaaaactgc tctaagacaa gcaagaaggg agacctacta aatgcccatt 200
atgacggcta cctggctaaa gacggctcga aattctactg cagccggaca 250
caaaaatgaag gccaccccaa atggtttgtt cttggtgttgg caagtcata 300
aaaaggccta gacattgcta tgacagatata gtgcctgga gaaaagcgaa 350
aagtagttat acccccttca tttgcatacg gaaaggaagg ctatgcagaa 400

ggcaagattc caccggatgc tacattgatt tttgagattt aactttatgc 450
tgtgacaaa ggaccacgga gcattgagac atttaaacaat atagacatgg 500
acaatgacag gcagctctct aaagccgaga taaacctcta cttgcaaagg 550
gaatttgaaa aagatgagaa gccacgtgac aagtcatatc aggatgcagt 600
tttagaagat atttttaaga agaatgacca tgatggtgat ggcttcattt 650
ctcccaagga atacaatgta taccaacacg atgaactata gcataattgt 700
atttctactt tttttttta gctatttact gtactttatg tataaaacaat 750
agtcactttt ctccaagttt tatttgctat ttttccctta tgagaagata 800
ttttgatctc cccaatacat tgattttggt ataataaaatg tgaggctgtt 850
ttgcaaacctt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 900
aaaaaaaa 907

<210> 180

<211> 222

<212> PRT

<213> Homo sapiens

<400> 180

Met	Pro	Lys	Thr	Met	His	Phe	Leu	Phe	Arg	Phe	Ile	Val	Phe	Phe
1				5					10					15

Tyr	Leu	Trp	Gly	Leu	Phe	Thr	Ala	Gln	Arg	Gln	Lys	Lys	Glu	Glu
				20					25					30

Ser	Thr	Glu	Glu	Val	Lys	Ile	Glu	Val	Leu	His	Arg	Pro	Glu	Asn
				35					40					45

Cys	Ser	Lys	Thr	Ser	Lys	Lys	Gly	Asp	Leu	Leu	Asn	Ala	His	Tyr
					50				55					60

Asp	Gly	Tyr	Leu	Ala	Lys	Asp	Gly	Ser	Lys	Phe	Tyr	Cys	Ser	Arg
				65					70					75

Thr	Gln	Asn	Glu	Gly	His	Pro	Lys	Trp	Phe	Val	Leu	Gly	Val	Gly
				80					85					90

Gln	Val	Ile	Lys	Gly	Leu	Asp	Ile	Ala	Met	Thr	Asp	Met	Cys	Pro
					95				100					105

Gly	Glu	Lys	Arg	Lys	Val	Val	Ile	Pro	Pro	Ser	Phe	Ala	Tyr	Gly
					110			115						120

Lys	Glu	Gly	Tyr	Ala	Glu	Gly	Lys	Ile	Pro	Pro	Asp	Ala	Thr	Leu
					125				130					135

Ile	Phe	Glu	Ile	Glu	Leu	Tyr	Ala	Val	Thr	Lys	Gly	Pro	Arg	Ser
					140				145					150

Ile Glu Thr Phe Lys Gln Ile Asp Met Asp Asn Asp Arg Gln Leu
155 160 165

Ser Lys Ala Glu Ile Asn Leu Tyr Leu Gln Arg Glu Phe Glu Lys
170 175 180

Asp Glu Lys Pro Arg Asp Lys Ser Tyr Gln Asp Ala Val Leu Glu
185 190 195

Asp Ile Phe Lys Lys Asn Asp His Asp Gly Asp Gly Phe Ile Ser
200 205 210

Pro Lys Glu Tyr Asn Val Tyr Gln His Asp Glu Leu
215 220

<210> 181
<211> 22
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-22
<223> Synthetic construct.

<400> 181
gtgttctgct ggagccgatg cc 22

<210> 182
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 182
gacatggaca atgacagg 18

<210> 183
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 183
cctttcagga tgtaggag 18

<210> 184
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 184
gatgtctgcc accccaag 18

<210> 185
<211> 27
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-27
<223> Synthetic construct.

<400> 185
gcattcctgat atgacttgtc acgtggc 27

<210> 186
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 186
tacaagaggg aagaggagtt gcac 24

<210> 187
<211> 52
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-52
<223> Synthetic construct.

<400> 187
ggccattatg acggctacct ggctaaagac ggctcgaaat tctactgcag 50

cc 52

<210> 188
<211> 573
<212> DNA
<213> Homo sapiens

<400> 188
cagaaatgca gggaccattg cttcttcag gcctctgctt tctgctgagc 50
ctctttggag ctgtgactca gaaaacccaaa acttcctgtg ctaagtgcc 100

cccaaatgct tcctgtgtca ataacactca ctgcacctgc aaccatggat 150
atacttctgg atctggcag aaactattca cattccctt ggagacatgt 200
aacgccaggc atggcgtc gcgcctgtaa tcccagtct ttggaaagcc 250
aaggcaggta gatcacctga ggtcaggagt ttgagaccag cctggccaac 300
atagtgaaac cccgtgtcta ctaaaaatac aaaaatcagc cgggcgtgg 350
ggtgcattgc tgcaatcca gttactcgaa aggctgaggc aggagaatcg 400
cttgaactca ggaggcagaa gttgcagtga acccagatcc tgccattgca 450
ctccagcatg gatgacagag caagactccg tctaaaaaag aaaagatagt 500
ttcttgtttc atttcgac tgccctctca gtgttcctg ggatcccc 550
ccaaataaag tacttatatt ctc 573

<210> 189

<211> 74

<212> PRT

<213> Homo sapiens

<400> 189

Met Gln Gly Pro Leu Leu Leu Pro Gly Leu Cys Phe Leu Leu Ser
1 5 10 15

Leu Phe Gly Ala Val Thr Gln Lys Thr Lys Thr Ser Cys Ala Lys
20 25 30

Cys Pro Pro Asn Ala Ser Cys Val Asn Asn Thr His Cys Thr Cys
35 40 45

Asn His Gly Tyr Thr Ser Gly Ser Gly Gln Lys Leu Phe Thr Phe
50 55 60

Pro Leu Glu Thr Cys Asn Ala Arg His Gly Gly Ser Arg Leu
65 70

<210> 190

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 190

agggaccatt gcttcttcca ggcc 24

<210> 191

<211> 24

<212> DNA

<213> Artificial

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<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 191
cgttacatgt ctccaagggg aatg 24

<210> 192
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 192
cctgtgctaa gtgcccccc aatgcttcct gtgtcaataa cactcactgc 50

<210> 193
<211> 1091
<212> DNA
<213> Homo sapiens

<400> 193
caaggcaggc atccccttgg tgaccttcaa agagaagcag agagggcaga 50
ggtgtggggc acaggaaag ggtgacctct gagattcccc ttttcccca 100
gactttggaa gtgaccaccatgggctca gcatctttt gctcctgtgt 150
gttcttgggc tcagccaggc agccacaccc aagatttca atggcactga 200
gtgtggcgt aactcacagc cgtggcaggt ggggctgttt gagggcacca 250
gcctgcgctg cgggggtgtc cttattgacc acaggtgggt cctcacagcg 300
gctcaactgca gcggcagcag gtactgggt cgccctgggg aacacagcct 350
cagccagctc gactggaccg agcagatccg gcacagcggc ttctctgtga 400
cccatcccg ctacctggga gcctcgacga gccacgagca cgacctccgg 450
ctgctgcggc tgcgcctgcc cgtccgcgtta accagcagcg ttcaacccct 500
gcccctgcggc aatgactgtg caaccgcgtt caccgagtgc cacgtctcag 550
gctggggcat caccaaccac ccacggAACCC cattcccgga tctgctccag 600
tgcctcaacc tctccatcgt ctcccatgcc acctgcgtatg gtgtgtatcc 650
cgggagaatc acgagcaaca tggtgtgtgc aggccgcgtc ccggggcagg 700
atgcctgcca gggtgattct gggggccccc tgggtgtgtgg gggagtcctt 750
caagggtctgg tgtcctgggg gtctgtgggg ccctgtggac aagatggcat 800

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ccctggagtc tacacctata tttgcaagta tgtggactgg atccggatga 850
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ccctagctcc actcttgttg gcctggAAC ttcttggAAC tttaactcct 1000
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<210> 194

<211> 248

<212> PRT

<213> Homo sapiens

<400> 194

Met Gly Leu Ser Ile Phe Leu Leu Cys Val Leu Gly Leu Ser
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Gln Ala Ala Thr Pro Lys Ile Phe Asn Gly Thr Glu Cys Gly Arg
20 25 30

Asn Ser Gln Pro Trp Gln Val Gly Leu Phe Glu Gly Thr Ser Leu
35 40 45

Arg Cys Gly Gly Val Leu Ile Asp His Arg Trp Val Leu Thr Ala
50 55 60

Ala His Cys Ser Gly Ser Arg Tyr Trp Val Arg Leu Gly Glu His
65 70 75

Ser Leu Ser Gln Leu Asp Trp Thr Glu Gln Ile Arg His Ser Gly
80 85 90

Phe Ser Val Thr His Pro Gly Tyr Leu Gly Ala Ser Thr Ser His
95 100 105

Glu His Asp Leu Arg Leu Leu Arg Leu Arg Leu Pro Val Arg Val
110 115 120

Thr Ser Ser Val Gln Pro Leu Pro Leu Pro Asn Asp Cys Ala Thr
125 130 135

Ala Gly Thr Glu Cys His Val Ser Gly Trp Gly Ile Thr Asn His
140 145 150

Pro Arg Asn Pro Phe Pro Asp Leu Leu Gln Cys Leu Asn Leu Ser
155 160 165

Ile Val Ser His Ala Thr Cys His Gly Val Tyr Pro Gly Arg Ile
170 175 180

Thr Ser Asn Met Val Cys Ala Gly Gly Val Pro Gly Gln Asp Ala
185 190 195

Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Gly Val Leu

200	205	210
Gln Gly Leu Val Ser Trp Gly Ser Val Gly Pro Cys Gly Gln Asp		
215	220	225
Gly Ile Pro Gly Val Tyr Thr Tyr Ile Cys Lys Tyr Val Asp Trp		
230	235	240
Ile Arg Met Ile Met Arg Asn Asn		
245		

<210> 195
<211> 1485
<212> DNA
<213> Homo sapiens

<400> 195
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ggcttgctca aagcccgca ggagaggagg ctggccgaga tcaaccggga 200
gtttctgtgt gaccagaagt acagtgtatga agagaacctt ccagaaaagc 250
tcacagcctt caaagagaag tacatggagt ttgacactgaa caatgaaggc 300
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tgaccccaat ctgcttgaaa aaaaaaaaaa aaaaaa 1485

<210> 196

<211> 150

<212> PRT

<213> Homo sapiens

<400> 196

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Gly Leu Leu Lys Ala Arg Gln Glu Arg Arg Leu Ala Glu Ile Asn
20 25 30

Arg Glu Phe Leu Cys Asp Gln Lys Tyr Ser Asp Glu Glu Asn Leu
35 40 45

Pro Glu Lys Leu Thr Ala Phe Lys Glu Lys Tyr Met Glu Phe Asp
50 55 60

Leu Asn Asn Glu Gly Glu Ile Asp Leu Met Ser Leu Lys Arg Met
65 70 75

Met Glu Lys Leu Gly Val Pro Lys Thr His Leu Glu Met Lys Lys
80 85 90

Met Ile Ser Glu Val Thr Gly Gly Val Ser Asp Thr Ile Ser Tyr
95 100 105

Arg Asp Phe Val Asn Met Met Leu Gly Lys Arg Ser Ala Val Leu
110 115 120

Lys Leu Val Met Met Phe Glu Gly Lys Ala Asn Glu Ser Ser Pro
125 130 135

Lys Pro Val Gly Pro Pro Pro Glu Arg Asp Ile Ala Ser Leu Pro
140 145 150

<210> 197

<211> 4842

<212> DNA

<213> Homo sapiens

<400> 197
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<210> 198

<211> 1523

<212> PRT

<213> Homo sapiens

<400> 198

Met	Ala	Pro	Gly	Trp	Ala	Gly	Val	Gly	Ala	Ala	Val	Arg	Ala	Arg
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Leu	Ala	Leu	Ala	Leu	Ala	Leu	Ala	Ser	Val	Leu	Ser	Gly	Pro	Pro
				20					25			30		
Ala	Val	Ala	Cys	Pro	Thr	Lys	Cys	Thr	Cys	Ser	Ala	Ala	Ser	Val
			35					40			45			
Asp	Cys	His	Gly	Leu	Gly	Leu	Arg	Ala	Val	Pro	Arg	Gly	Ile	Pro
				50					55			60		
Arg	Asn	Ala	Glu	Arg	Leu	Asp	Leu	Asp	Arg	Asn	Asn	Ile	Thr	Arg
				65					70			75		
Ile	Thr	Lys	Met	Asp	Phe	Ala	Gly	Leu	Lys	Asn	Leu	Arg	Val	Leu
			80						85			90		
His	Leu	Glu	Asp	Asn	Gln	Val	Ser	Val	Ile	Glu	Arg	Gly	Ala	Phe
				95					100			105		
Gln	Asp	Leu	Lys	Gln	Leu	Glu	Arg	Leu	Arg	Leu	Asn	Lys	Asn	Lys
				110					115			120		
Leu	Gln	Val	Leu	Pro	Glu	Leu	Leu	Phe	Gln	Ser	Thr	Pro	Lys	Leu
				125					130			135		
Thr	Arg	Leu	Asp	Leu	Ser	Glu	Asn	Gln	Ile	Gln	Gly	Ile	Pro	Arg
				140					145			150		
Lys	Ala	Phe	Arg	Gly	Ile	Thr	Asp	Val	Lys	Asn	Leu	Gln	Leu	Asp
				155					160			165		

Asn Asn His Ile Ser Cys Ile Glu Asp Gly Ala Phe Arg Ala Leu
 170 175 180
 Arg Asp Leu Glu Ile Leu Thr Leu Asn Asn Asn Asn Ile Ser Arg
 185 190 195
 Ile Leu Val Thr Ser Phe Asn His Met Pro Lys Ile Arg Thr Leu
 200 205 210
 Arg Leu His Ser Asn His Leu Tyr Cys Asp Cys His Leu Ala Trp
 215 220 225
 Leu Ser Asp Trp Leu Arg Gln Arg Arg Thr Val Gly Gln Phe Thr
 230 235 240
 Leu Cys Met Ala Pro Val His Leu Arg Gly Phe Asn Val Ala Asp
 245 250 255
 Val Gln Lys Lys Glu Tyr Val Cys Pro Ala Pro His Ser Glu Pro
 260 265 270
 Pro Ser Cys Asn Ala Asn Ser Ile Ser Cys Pro Ser Pro Cys Thr
 275 280 285
 Cys Ser Asn Asn Ile Val Asp Cys Arg Gly Lys Gly Leu Met Glu
 290 295 300
 Ile Pro Ala Asn Leu Pro Glu Gly Ile Val Glu Ile Arg Leu Glu
 305 310 315
 Gln Asn Ser Ile Lys Ala Ile Pro Ala Gly Ala Phe Thr Gln Tyr
 320 325 330
 Lys Lys Leu Lys Arg Ile Asp Ile Ser Lys Asn Gln Ile Ser Asp
 335 340 345
 Ile Ala Pro Asp Ala Phe Gln Gly Leu Lys Ser Leu Thr Ser Leu
 350 355 360
 Val Leu Tyr Gly Asn Lys Ile Thr Glu Ile Ala Lys Gly Leu Phe
 365 370 375
 Asp Gly Leu Val Ser Leu Gln Leu Leu Leu Leu Asn Ala Asn Lys
 380 385 390
 Ile Asn Cys Leu Arg Val Asn Thr Phe Gln Asp Leu Gln Asn Leu
 395 400 405
 Asn Leu Leu Ser Leu Tyr Asp Asn Lys Leu Gln Thr Ile Ser Lys
 410 415 420
 Gly Leu Phe Ala Pro Leu Gln Ser Ile Gln Thr Leu His Leu Ala
 425 430 435
 Gln Asn Pro Phe Val Cys Asp Cys His Leu Lys Trp Leu Ala Asp
 440 445 450
 Tyr Leu Gln Asp Asn Pro Ile Glu Thr Ser Gly Ala Arg Cys Ser

455	460	465
Ser Pro Arg Arg Leu Ala Asn Lys Arg Ile Ser Gln Ile Lys Ser		
470	475	480
Lys Lys Phe Arg Cys Ser Gly Ser Glu Asp Tyr Arg Ser Arg Phe		
485	490	495
Ser Ser Glu Cys Phe Met Asp Leu Val Cys Pro Glu Lys Cys Arg		
500	505	510
Cys Glu Gly Thr Ile Val Asp Cys Ser Asn Gln Lys Leu Val Arg		
515	520	525
Ile Pro Ser His Leu Pro Glu Tyr Val Thr Asp Leu Arg Leu Asn		
530	535	540
Asp Asn Glu Val Ser Val Leu Glu Ala Thr Gly Ile Phe Lys Lys		
545	550	555
Leu Pro Asn Leu Arg Lys Ile Asn Leu Ser Asn Asn Lys Ile Lys		
560	565	570
Glu Val Arg Glu Gly Ala Phe Asp Gly Ala Ala Ser Val Gln Glu		
575	580	585
Leu Met Leu Thr Gly Asn Gln Leu Glu Thr Val His Gly Arg Val		
590	595	600
Phe Arg Gly Leu Ser Gly Leu Lys Thr Leu Met Leu Arg Ser Asn		
605	610	615
Leu Ile Ser Cys Val Ser Asn Asp Thr Phe Ala Gly Leu Ser Ser		
620	625	630
Val Arg Leu Leu Ser Leu Tyr Asp Asn Arg Ile Thr Thr Ile Thr		
635	640	645
Pro Gly Ala Phe Thr Thr Leu Val Ser Leu Ser Thr Ile Asn Leu		
650	655	660
Leu Ser Asn Pro Phe Asn Cys Asn Cys His Leu Ala Trp Leu Gly		
665	670	675
Lys Trp Leu Arg Lys Arg Arg Ile Val Ser Gly Asn Pro Arg Cys		
680	685	690
Gln Lys Pro Phe Phe Leu Lys Glu Ile Pro Ile Gln Asp Val Ala		
695	700	705
Ile Gln Asp Phe Thr Cys Asp Gly Asn Glu Glu Ser Ser Cys Gln		
710	715	720
Leu Ser Pro Arg Cys Pro Glu Gln Cys Thr Cys Met Glu Thr Val		
725	730	735
Val Arg Cys Ser Asn Lys Gly Leu Arg Ala Leu Pro Arg Gly Met		
740	745	750

Pro Lys Asp Val Thr Glu Leu Tyr Leu Glu Gly Asn His Leu Thr
 755 760 765
 Ala Val Pro Arg Glu Leu Ser Ala Leu Arg His Leu Thr Leu Ile
 770 775 780
 Asp Leu Ser Asn Asn Ser Ile Ser Met Leu Thr Asn Tyr Thr Phe
 785 790 795
 Ser Asn Met Ser His Leu Ser Thr Leu Ile Leu Ser Tyr Asn Arg
 800 805 810
 Leu Arg Cys Ile Pro Val His Ala Phe Asn Gly Leu Arg Ser Leu
 815 820 825
 Arg Val Leu Thr Leu His Gly Asn Asp Ile Ser Ser Val Pro Glu
 830 835 840
 Gly Ser Phe Asn Asp Leu Thr Ser Leu Ser His Leu Ala Leu Gly
 845 850 855
 Thr Asn Pro Leu His Cys Asp Cys Ser Leu Arg Trp Leu Ser Glu
 860 865 870
 Trp Val Lys Ala Gly Tyr Lys Glu Pro Gly Ile Ala Arg Cys Ser
 875 880 885
 Ser Pro Glu Pro Met Ala Asp Arg Leu Leu Leu Thr Thr Pro Thr
 890 895 900
 His Arg Phe Gln Cys Lys Gly Pro Val Asp Ile Asn Ile Val Ala
 905 910 915
 Lys Cys Asn Ala Cys Leu Ser Ser Pro Cys Lys Asn Asn Gly Thr
 920 925 930
 Cys Thr Gln Asp Pro Val Glu Leu Tyr Arg Cys Ala Cys Pro Tyr
 935 940 945
 Ser Tyr Lys Gly Lys Asp Cys Thr Val Pro Ile Asn Thr Cys Ile
 950 955 960
 Gln Asn Pro Cys Gln His Gly Gly Thr Cys His Leu Ser Asp Ser
 965 970 975
 His Lys Asp Gly Phe Ser Cys Ser Cys Pro Leu Gly Phe Glu Gly
 980 985 990
 Gln Arg Cys Glu Ile Asn Pro Asp Asp Cys Glu Asp Asn Asp Cys
 995 1000 1005
 Glu Asn Asn Ala Thr Cys Val Asp Gly Ile Asn Asn Tyr Val Cys
 1010 1015 1020
 Ile Cys Pro Pro Asn Tyr Thr Gly Glu Leu Cys Asp Glu Val Ile
 1025 1030 1035
 Asp His Cys Val Pro Glu Leu Asn Leu Cys Gln His Glu Ala Lys

1040	1045	1050
Cys Ile Pro Leu Asp Lys Gly Phe Ser Cys Glu Cys Val Pro Gly 1055	1060	1065
Tyr Ser Gly Lys Leu Cys Glu Thr Asp Asn Asp Asp Cys Val Ala 1070	1075	1080
His Lys Cys Arg His Gly Ala Gln Cys Val Asp Thr Ile Asn Gly 1085	1090	1095
Tyr Thr Cys Thr Cys Pro Gln Gly Phe Ser Gly Pro Phe Cys Glu 1100	1105	1110
His Pro Pro Pro Met Val Leu Leu Gln Thr Ser Pro Cys Asp Gln 1115	1120	1125
Tyr Glu Cys Gln Asn Gly Ala Gln Cys Ile Val Val Gln Gln Glu 1130	1135	1140
Pro Thr Cys Arg Cys Pro Pro Gly Phe Ala Gly Pro Arg Cys Glu 1145	1150	1155
Lys Leu Ile Thr Val Asn Phe Val Gly Lys Asp Ser Tyr Val Glu 1160	1165	1170
Leu Ala Ser Ala Lys Val Arg Pro Gln Ala Asn Ile Ser Leu Gln 1175	1180	1185
Val Ala Thr Asp Lys Asp Asn Gly Ile Leu Leu Tyr Lys Gly Asp 1190	1195	1200
Asn Asp Pro Leu Ala Leu Glu Leu Tyr Gln Gly His Val Arg Leu 1205	1210	1215
Val Tyr Asp Ser Leu Ser Ser Pro Pro Thr Thr Val Tyr Ser Val 1220	1225	1230
Glu Thr Val Asn Asp Gly Gln Phe His Ser Val Glu Leu Val Thr 1235	1240	1245
Leu Asn Gln Thr Leu Asn Leu Val Val Asp Lys Gly Thr Pro Lys 1250	1255	1260
Ser Leu Gly Lys Leu Gln Lys Gln Pro Ala Val Gly Ile Asn Ser 1265	1270	1275
Pro Leu Tyr Leu Gly Gly Ile Pro Thr Ser Thr Gly Leu Ser Ala 1280	1285	1290
Leu Arg Gln Gly Thr Asp Arg Pro Leu Gly Gly Phe His Gly Cys 1295	1300	1305
Ile His Glu Val Arg Ile Asn Asn Glu Leu Gln Asp Phe Lys Ala 1310	1315	1320
Leu Pro Pro Gln Ser Leu Gly Val Ser Pro Gly Cys Lys Ser Cys 1325	1330	1335

Thr Val Cys Lys His Gly Leu Cys Arg Ser Val Glu Lys Asp Ser
 1340 1345 1350
 Val Val Cys Glu Cys Arg Pro Gly Trp Thr Gly Pro Leu Cys Asp
 1355 1360 1365
 Gln Glu Ala Arg Asp Pro Cys Leu Gly His Arg Cys His His Gly
 1370 1375 1380
 Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu
 1385 1390 1395
 Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser Ala Asn
 1400 1405 1410
 Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser
 1415 1420 1425
 Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly
 1430 1435 1440
 Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg
 1445 1450 1455
 Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala Thr Ala
 1460 1465 1470
 Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro Gln
 1475 1480 1485
 Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln
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 Glu Cys Gly Cys Leu Ala Cys Ser
 1520

<210> 199

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 199

atggagatcc ctgccaactt gccg 24

<210> 200

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 200
ttgttggcat tgaggaggag cagc 24

<210> 201
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 201
gagggcatacg tcgaaatacg cctagaacag aactccatca aagccatccc 50

<210> 202
<211> 753
<212> DNA
<213> Homo sapiens

<400> 202
ggatgcagga cgctccctg agctgcctgt caccgactag gtggagcagt 50
gtttcttcgg cagactcaac tgagaagtca gcctctgggg caggcaccag 100
gaatctgcct tttcagttct gtctccggca ggcttgagg atgaaggctg 150
cggcattct gaccctcatt ggctgcctgg tcacaggcgc cgagtccaaa 200
atctacactc gttgcaaact ggcaaaaata ttctcgaggg ctggcctgga 250
caattactgg ggcttcagcc ttggaaaactg gatctgcatt gcatattatg 300
agagcggcta caacaccaca gccccgacgg tcctggatga cggcagcattc 350
gactatggca tcttcagat caacagcttc gcgtggtgca gacgcggaaa 400
gctgaaggag aacaaccact gccatgtcgc ctgctcagcc ttgatcactg 450
atgacacctac agatgcaatt atctgtgcac ggaaaattgt taaagagaca 500
caaggaatga actattggca aggctggaaag aaacattgtg agggcagaga 550
cctgtccgag tggaaaaaaag gctgtgaggt ttccctaaact ggaactggac 600
ccaggatgtt ttgcagcaac gcccttaggat ttgcagtgaa tgtccaaatg 650
cctgtgtcat cttgtcccgat ttccctccaa tattcattct caaacttgaa 700
gagggaaaat taagctatac ttttaagaaa ataaatattt ccatttaaat 750
gtc 753

<210> 203
<211> 148
<212> PRT
<213> Homo sapiens

<400> 203
Met Lys Ala Ala Gly Ile Leu Thr Leu Ile Gly Cys Leu Val Thr
1 5 10 15
Gly Ala Glu Ser Lys Ile Tyr Thr Arg Cys Lys Leu Ala Lys Ile
20 25 30
Phe Ser Arg Ala Gly Leu Asp Asn Tyr Trp Gly Phe Ser Leu Gly
35 40 45
Asn Trp Ile Cys Met Ala Tyr Tyr Glu Ser Gly Tyr Asn Thr Thr
50 55 60
Ala Pro Thr Val Leu Asp Asp Gly Ser Ile Asp Tyr Gly Ile Phe
65 70 75
Gln Ile Asn Ser Phe Ala Trp Cys Arg Arg Gly Lys Leu Lys Glu
80 85 90
Asn Asn His Cys His Val Ala Cys Ser Ala Leu Ile Thr Asp Asp
95 100 105
Leu Thr Asp Ala Ile Ile Cys Ala Arg Lys Ile Val Lys Glu Thr
110 115 120
Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys Glu Gly
125 130 135
Arg Asp Leu Ser Glu Trp Lys Lys Gly Cys Glu Val Ser
140 145

<210> 204
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 204
gcaggcttg aggatgaagg ctgc 24

<210> 205
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 205
ctcattggct gcctggtcac aggc 24

<210> 206
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 206
ccagtcggac aggtctctcc cctc 24

<210> 207
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 207
tcagtgacca aggctgagca ggcg 24

<210> 208
<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 208
ctacactcgt tgcaaactgg caaaaatatt ctcgagggt ggcctgg 47

<210> 209
<211> 1648
<212> DNA
<213> Homo sapiens

<400> 209
caggccattt gcatcccact gtccttgtgt tcggagccag gccacaccgt 50
cctcagcagt gtcatgtgtt aaaaacgcca agctgaatat atcatcccc 100
tattaaaaact tgtacatggc tccccattgg tttttggaga aaagttcaag 150
ctttttacct tggtgtctgc ctgtatccca gtgttcaggc tggctagacg 200
gcggaagaag atcctatattt actgtcactt cccagatctg cttctcacca 250

agagagattc ttttcttaaa cgactataca gggccccaat tgactggata 300
gaggaataca ccacaggcat ggcagactgc atcttagtca acagccagtt 350
cacagctgct gttttaagg aaacattcaa gtccctgtct cacatagacc 400
ctgatgtcct ctatccatct ctaaatgtca ccagcttga ctcagttgtt 450
cctgaaaagc tggatgacct agtccccaaag gggaaaaaat tcctgctgct 500
ctccatcaac agatacgaaa ggaagaaaaa tctgactttg gcactggaag 550
ccctagtaca gctgcgtgga agattgacat cccaaagattg ggagagggtt 600
catctgatcg tggcaggtgg ttatgacgag agagtcctgg agaatgtgga 650
acattatcag gaattgaaga aaatggtcca acagtccgac cttggccagt 700
atgtgacctt cttgaggtct ttctcagaca aacagaaaaat ctccctcctc 750
cacagctgca cgtgtgtgct ttacacacca agcaatgagc actttggcat 800
tgtccctctg gaagccatgt acatgcagtg cccagtcatt gctgttaatt 850
cgggtggacc cttggagtcc attgaccaca gtgtcacagg gtttctgtgt 900
gagcctgacc cggcgcactt ctcagaagca atagaaaaagt tcatccgtga 950
accttcctta aaagccacca tgggcctggc tggaagagcc agagtgaagg 1000
aaaaattttc ccctgaagca tttacagaac agctctaccg atatgttacc 1050
aaactgctgg tataatcaga ttgttttaa gatctccatt aatgtcattt 1100
ttatggattt tagacccagt tttgaaacca aaaaagaaac ctagaatcta 1150
atgcagaaga gatctttaa aaaataaact tgagtcttga atgtgagcca 1200
ctttcctata taccacaccc ccctgtccac ttttcagaaa aaccatgtct 1250
tttatgctat aatcattcca aattttgccca gtgttaagtt acaaatgtgg 1300
tgtcattcca tgttcagcag agtattttaa ttatatttc tcgggattat 1350
tgctcttctg tctataaatt ttgaatgata ctgtgcctta attggtttc 1400
atagtttaag tgtgtatcat tatcaaagtt gattaatttgc ttcatagt 1450
ataatgagag cagggctatt gtatcccatt gattcaatcc accgaagtgt 1500
tcactgtcat ctgttaggaa atttttgttt gtcctgtctt tgccctggatc 1550
catagcgaga gtgcctgtta ttttttttaa gataatttgtt atttttgcac 1600
actgagat aataaaaggt gtttatcata aaaaaaaaaa aaaaaaaaaa 1648

<210> 210
<211> 323

<212> PRT

<213> Homo sapiens

<400> 210

Met	Pro	Leu	Leu	Lys	Leu	Val	His	Gly	Ser	Pro	Leu	Val	Phe	Gly
1				5				10					15	
Glu	Lys	Phe	Lys	Leu	Phe	Thr	Leu	Val	Ser	Ala	Cys	Ile	Pro	Val
				20				25					30	
Phe	Arg	Leu	Ala	Arg	Arg	Arg	Lys	Lys	Ile	Leu	Phe	Tyr	Cys	His
				35				40					45	
Phe	Pro	Asp	Leu	Leu	Leu	Thr	Lys	Arg	Asp	Ser	Phe	Leu	Lys	Arg
				50				55					60	
Leu	Tyr	Arg	Ala	Pro	Ile	Asp	Trp	Ile	Glu	Glu	Tyr	Thr	Thr	Gly
				65				70					75	
Met	Ala	Asp	Cys	Ile	Leu	Val	Asn	Ser	Gln	Phe	Thr	Ala	Ala	Val
				80				85					90	
Phe	Lys	Glu	Thr	Phe	Lys	Ser	Leu	Ser	His	Ile	Asp	Pro	Asp	Val
				95				100					105	
Leu	Tyr	Pro	Ser	Leu	Asn	Val	Thr	Ser	Phe	Asp	Ser	Val	Val	Pro
				110				115					120	
Glu	Lys	Leu	Asp	Asp	Leu	Val	Pro	Lys	Gly	Lys	Lys	Phe	Leu	Leu
				125				130					135	
Leu	Ser	Ile	Asn	Arg	Tyr	Glu	Arg	Lys	Lys	Asn	Leu	Thr	Leu	Ala
				140				145					150	
Leu	Glu	Ala	Leu	Val	Gln	Leu	Arg	Gly	Arg	Leu	Thr	Ser	Gln	Asp
				155				160					165	
Trp	Glu	Arg	Val	His	Leu	Ile	Val	Ala	Gly	Gly	Tyr	Asp	Glu	Arg
				170				175					180	
Val	Leu	Glu	Asn	Val	Glu	His	Tyr	Gln	Glu	Leu	Lys	Lys	Met	Val
				185				190					195	
Gln	Gln	Ser	Asp	Leu	Gly	Gln	Tyr	Val	Thr	Phe	Leu	Arg	Ser	Phe
				200				205					210	
Ser	Asp	Lys	Gln	Lys	Ile	Ser	Leu	Leu	His	Ser	Cys	Thr	Cys	Val
				215				220					225	
Leu	Tyr	Thr	Pro	Ser	Asn	Glu	His	Phe	Gly	Ile	Val	Pro	Leu	Glu
				230				235					240	
Ala	Met	Tyr	Met	Gln	Cys	Pro	Val	Ile	Ala	Val	Asn	Ser	Gly	Gly
				245				250					255	
Pro	Leu	Glu	Ser	Ile	Asp	His	Ser	Val	Thr	Gly	Phe	Leu	Cys	Glu
				260				265					270	

Pro Asp Pro Val His Phe Ser Glu Ala Ile Glu Lys Phe Ile Arg
 275 280 285
 Glu Pro Ser Leu Lys Ala Thr Met Gly Leu Ala Gly Arg Ala Arg
 290 295 300
 Val Lys Glu Lys Phe Ser Pro Glu Ala Phe Thr Glu Gln Leu Tyr
 305 310 315
 Arg Tyr Val Thr Lys Leu Leu Val
 320

<210> 211
 <211> 1554
 <212> DNA
 <213> Homo sapiens

<400> 211
 gactacgccc atccgagacg tggctccctg ggccggcagaa ccatgttgg 50
 cttcgcgatc ttccgcgtta ctttcttgct ggcgttgg 50 100
 tctacctcta tccggcttcc agacaagctg caggaattcc agggattact 150
 ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtggaa 200
 tttgcatgag ttccctgg 50 ttgcatgaa gagatatgg cctgtgg 50 250
 ctttctgg 50 tggcaggcgc ctcgtgg 50 gtttggcac tggtgatgta 300
 ctgaaggcagc atatcaatcc caataagaca tcggaccctt ttgaaaccat 350
 gctgaagtca ttatcgatgg atcaatctgg tgggtggcagt gtgagtgaaa 400
 accacatgag gaaaaaattt 50 tatgaaaatg gtgtgactga ttctctgaag 450
 agtaactttg ccctccctt 50 aaagcttca gaagaattat tagataatg 500
 gctctcctac ccagagaccc agcacgtgcc cctcagccag catatgctt 550
 gttttgttat 50 gaagtctgtt acacagatgg taatgggttag tacatgg 600
 gatgatcagg aagtcatcg cttccagaag aatcatggca cagttggc 650
 tgagattgga aaaggcttc tagatggc acttgataaa aacatgactc 700
 gaaaaaaaca atatgaagat gccctcatgc aactggagtc tggtttaagg 750
 aacatcataa aagaacgaaa aggaaggaac ttcaatgcac atatttcat 800
 tgactcctta gtacaaggaa accttaatga ccaacagatc ctagaagaca 850
 gtatgatatt ttctctggcc agttgcataa taactgcaaa attgtgtacc 900
 tgggcaatct gtttttaac cacctctgaa gaagttcaaa aaaaattata 950
 tgaagagata aaccaagttt ttggaaatgg tcctgttact ccagagaaaa 1000

ttgagcagct cagatattgt cagcatgtgc tttgtgaac tgttcgaact 1050
gccaaactga ctccagttc tgcccagctt caagatattg aaggaaaaat 1100
tgaccgatt attattccta gagagaccct cgtccttat gcccttggtg 1150
tggtaactca ggatccta atctggccat ctccacacaa gtttgatcca 1200
gatcggtttg atgatgaatt agtaatgaaa acttttcct cacttggatt 1250
ctcaggcaca caggagtgtc cagagttgag gtttgcataat atggtgacca 1300
cagtacttct tagtgttattt gtgaagagac tgcacctact ttctgtggag 1350
ggacaggtta ttgaaacaaa gtatgaactg gtaacatcat caagggaaaga 1400
agcttggatc actgtctcaa agagatatta aaatttata catttaaat 1450
cattgttaaa ttgattgagg aaaacaacca tttaaaaaaa atctatgtg 1500
aatccttta taaaccagta tcactttgta atataaacac ctatttgtac 1550
ttaa 1554

<210> 212
<211> 462
<212> PRT
<213> Homo sapiens

<400> 212
Met Leu Asp Phe Ala Ile Phe Ala Val Thr Phe Leu Leu Ala Leu
1 5 10 15
Val Gly Ala Val Leu Tyr Leu Tyr Pro Ala Ser Arg Gln Ala Ala
20 25 30
Gly Ile Pro Gly Ile Thr Pro Thr Glu Glu Lys Asp Gly Asn Leu
35 40 45
Pro Asp Ile Val Asn Ser Gly Ser Leu His Glu Phe Leu Val Asn
50 55 60
Leu His Glu Arg Tyr Gly Pro Val Val Ser Phe Trp Phe Gly Arg
65 70 75
Arg Leu Val Val Ser Leu Gly Thr Val Asp Val Leu Lys Gln His
80 85 90
Ile Asn Pro Asn Lys Thr Ser Asp Pro Phe Glu Thr Met Leu Lys
95 100 105
Ser Leu Leu Arg Tyr Gln Ser Gly Gly Gly Ser Val Ser Glu Asn
110 115 120
His Met Arg Lys Lys Leu Tyr Glu Asn Gly Val Thr Asp Ser Leu
125 130 135
Lys Ser Asn Phe Ala Leu Leu Lys Leu Ser Glu Glu Leu Leu

140	145	150
Asp Lys Trp Leu Ser Tyr Pro Glu Thr Gln His Val Pro Leu Ser		
155	160	165
Gln His Met Leu Gly Phe Ala Met Lys Ser Val Thr Gln Met Val		
170	175	180
Met Gly Ser Thr Phe Glu Asp Asp Gln Glu Val Ile Arg Phe Gln		
185	190	195
Lys Asn His Gly Thr Val Trp Ser Glu Ile Gly Lys Gly Phe Leu		
200	205	210
Asp Gly Ser Leu Asp Lys Asn Met Thr Arg Lys Lys Gln Tyr Glu		
215	220	225
Asp Ala Leu Met Gln Leu Glu Ser Val Leu Arg Asn Ile Ile Lys		
230	235	240
Glu Arg Lys Gly Arg Asn Phe Ser Gln His Ile Phe Ile Asp Ser		
245	250	255
Leu Val Gln Gly Asn Leu Asn Asp Gln Gln Ile Leu Glu Asp Ser		
260	265	270
Met Ile Phe Ser Leu Ala Ser Cys Ile Ile Thr Ala Lys Leu Cys		
275	280	285
Thr Trp Ala Ile Cys Phe Leu Thr Thr Ser Glu Glu Val Gln Lys		
290	295	300
Lys Leu Tyr Glu Glu Ile Asn Gln Val Phe Gly Asn Gly Pro Val		
305	310	315
Thr Pro Glu Lys Ile Glu Gln Leu Arg Tyr Cys Gln His Val Leu		
320	325	330
Cys Glu Thr Val Arg Thr Ala Lys Leu Thr Pro Val Ser Ala Gln		
335	340	345
Leu Gln Asp Ile Glu Gly Lys Ile Asp Arg Phe Ile Ile Pro Arg		
350	355	360
Glu Thr Leu Val Leu Tyr Ala Leu Gly Val Val Leu Gln Asp Pro		
365	370	375
Asn Thr Trp Pro Ser Pro His Lys Phe Asp Pro Asp Arg Phe Asp		
380	385	390
Asp Glu Leu Val Met Lys Thr Phe Ser Ser Leu Gly Phe Ser Gly		
395	400	405
Thr Gln Glu Cys Pro Glu Leu Arg Phe Ala Tyr Met Val Thr Thr		
410	415	420
Val Leu Leu Ser Val Leu Val Lys Arg Leu His Leu Leu Ser Val		
425	430	435

Glu Gly Gln Val Ile Glu Thr Lys Tyr Glu Leu Val Thr Ser Ser
440 445 450

Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg Tyr
455 460

<210> 213

<211> 759

<212> DNA

<213> Homo sapiens

<400> 213

ctagatttgt cggcttgcgg ggagacttca ggagtcgctg tctctgaact 50

tccagccctca gagaccgccc cccttgcctcc cgaggggccat gggccgggtc 100

tcagggcttg tgccctctcg ctccctgacg ctcctggcgc atctggtggt 150

cgtcatcacc ttattctggt cccggggacag caacatacag gcctgcctgc 200

ctctcacgtt cacccccgag gagtatgaca agcaggacat tcagctggtg 250

gccgcgcctct ctgtcaccct gggcctctt gcagtggagc tggccggttt 300

cctctcagga gtctccatgt tcaacagcac ccagagcctc atctccattg 350

gggctcactg tagtgcattcc gtggccctgt ctttcttcat attcgagcgt 400

tgggagtgca ctacgtattt gtacatttt gtcttctgca gtgcccttcc 450

agctgtcaact gaaatggctt tattcgtcac cgtctttggg ctgaaaaaga 500

aacccttctg attacctca tgacggAAC ctaaggacga agcctacagg 550

ggcaaggggcc gcttcgtatt cctggaaagaa ggaaggcata ggcttcgggt 600

ttccccctcgg aaactgcttc tgctggagga tatgtgttgg aataattacg 650

tcttgagtct gggattatcc gcattgtatt tagtgcattttaataaaaata 700

tgtttttagtag taacattaag acttatatac agtttttaggg gacaattaaa 750

aaaaaaaaaa 759

<210> 214

<211> 140

<212> PRT

<213> Homo sapiens

<400> 214

Met Gly Arg Val Ser Gly Leu Val Pro Ser Arg Phe Leu Thr Leu
1 5 10 15

Leu Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp
20 25 30

Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu
35 40 45

Tyr Asp Lys Gln Asp Ile Gln Leu Val Ala Ala Leu Ser Val Thr
50 55 60

Leu Gly Leu Phe Ala Val Glu Leu Ala Gly Phe Leu Ser Gly Val
65 70 75

Ser Met Phe Asn Ser Thr Gln Ser Leu Ile Ser Ile Gly Ala His
80 85 90

Cys Ser Ala Ser Val Ala Leu Ser Phe Phe Ile Phe Glu Arg Trp
95 100 105

Glu Cys Thr Thr Tyr Trp Tyr Ile Phe Val Phe Cys Ser Ala Leu
110 115 120

Pro Ala Val Thr Glu Met Ala Leu Phe Val Thr Val Phe Gly Leu
125 130 135

Lys Lys Lys Pro Phe
140

<210> 215

<211> 697

<212> DNA

<213> Homo sapiens

<400> 215

tcccgaccc tgccgcctg ccactatgtc ccgcgcctc atgctgcttg 50
cctggctct ccccagcctc ctgcactcg gagcggctca ggagacagaa 100
· gaccggcct gctcagccc catagtgccc cggaacgagt ggaaggccct 150
ggcatcagag tgcgcaggc acctgagcct gcccttacgc tatgtggtgg 200
tatcgcacac ggcggcagc agctgcaaca ccccgccctc gtgccagcag 250
caggccgga atgtcagca ctaccacatg aagacactgg gctggcgcga 300
cgtggctac aacttcctga ttggagaaga cgggctcgta tacgagggcc 350
gtggctggaa cttcacgggt gcccactcag gtcactätg gaacccatg 400
tccattggca tcagttcat gggcaactac atggatcggg tgcccacacc 450
ccaggccatc cggcagccc agggtctact ggcctgcggt gtggctcagg 500
gagccctgag gtccaaactat gtgctcaaag gacaccggga tgtgcagcgt 550
acactcttc cagggcaacca gcttaccac ctcatccaga attggccaca 600
ctaccgctcc ccctgaggcc ctgctgatcc gcacccatt cctccctcc 650
catggccaaa aaccccaactg tctccttctc caataaagat gtagctc 697

<210> 216

<211> 196

<212> PRT

<213> Homo sapiens

<400> 216

Met	Ser	Arg	Arg	Ser	Met	Leu	Leu	Ala	Trp	Ala	Leu	Pro	Ser	Leu
1					5				10					15
Leu	Arg	Leu	Gly	Ala	Ala	Gln	Glu	Thr	Glu	Asp	Pro	Ala	Cys	Cys
					20				25					30
Ser	Pro	Ile	Val	Pro	Arg	Asn	Glu	Trp	Lys	Ala	Leu	Ala	Ser	Glu
					35				40					45
Cys	Ala	Gln	His	Leu	Ser	Leu	Pro	Leu	Arg	Tyr	Val	Val	Val	Ser
					50				55					60
His	Thr	Ala	Gly	Ser	Ser	Cys	Asn	Thr	Pro	Ala	Ser	Cys	Gln	Gln
					65				70					75
Gln	Ala	Arg	Asn	Val	Gln	His	Tyr	His	Met	Lys	Thr	Leu	Gly	Trp
					80				85					90
Cys	Asp	Val	Gly	Tyr	Asn	Phe	Leu	Ile	Gly	Glu	Asp	Gly	Leu	Val
					95				100					105
Tyr	Glu	Gly	Arg	Gly	Trp	Asn	Phe	Thr	Gly	Ala	His	Ser	Gly	His
					110				115					120
Leu	Trp	Asn	Pro	Met	Ser	Ile	Gly	Ile	Ser	Phe	Met	Gly	Asn	Tyr
					125				130					135
Met	Asp	Arg	Val	Pro	Thr	Pro	Gln	Ala	Ile	Arg	Ala	Ala	Gln	Gly
					140				145					150
Leu	Leu	Ala	Cys	Gly	Val	Ala	Gln	Gly	Ala	Leu	Arg	Ser	Asn	Tyr
					155				160					165
Val	Leu	Lys	Gly	His	Arg	Asp	Val	Gln	Arg	Thr	Leu	Ser	Pro	Gly
					170				175					180
Asn	Gln	Leu	Tyr	His	Leu	Ile	Gln	Asn	Trp	Pro	His	Tyr	Arg	Ser
					185				190					195

Pro

<210> 217

<211> 1871

<212> DNA

<213> Homo sapiens

<400> 217

ctgggacccc gaaaaagagaa ggggagagcg aggggacgag agcggaggag 50
gaagatgcaa ctgactcgct gctgcttcgt gttccctggtg cagggttagcc 100
tctatcttgtt catctgtggc caggatgtat gtcctcccggtt ctcagaggac 150
cctgagcgtt atgaccacga gggccagccc cggccccggg tgcctcgaa 200

gcggggccac atctcaccta agtcccgc c catggccat tccactctcc 250
tagggctgct ggccccgcct ggggaggctt ggggcattct tgggcagccc 300
cccaaccgcc cgaaccacag ccccccaccc tcagccaagg tgaagaaaat 350
ctttggctgg ggcgacttct actccaacat caagacggtg gccctgaacc 400
tgctcgtcac aggaaagatt gtggaccatg gcaatggac cttcagcgtc 450
cacttccaac acaatgccac aggccaggg aacatctcca tcagccttgt 500
gccccccagt aaagctgttag agttccacca ggaacacgcag atcttcatcg 550
aagccaaggc ctccaaaatc ttcaactgcc ggatggagtg ggagaaggta 600
gaacggggcc gccggacctc gctttgcacc cacgaccagg ccaagatctg 650
ctcccgagac cacgctcaga gtcagccac ctggagctgc tcccagccct 700
tcaaagtctgt ctgtgtctac atcgcccttct acagcacgga ctatcggctg 750
gtccagaagg tgtgcccaga ttacaactac catagtgata cccctacta 800
cccatctggg tgaccgggg caggccacag aggccaggcc agggctggaa 850
ggacaggcct gcccatgcag gagaccatct ggacacccggg cagggaaagg 900
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gccaggggcca agtctcaagt ggcagagaaa gggtcccaag tgctggccc 1000
aacctgaagc tgtggagtga cttagatcaca ggagcactgg aggaggagtg 1050
ggctctctgt gcagcctcac agggcttgc cacggagcca cagagagatg 1100
ctgggtcccc gaggcctgtg ggcaggccga tcagtggtgc cccagatcaa 1150
gtcatggag gaagctaagc cttgggttct tgccatcctg agggaaagata 1200
gcaacaggga gggggagatt tcatcagtgt ggacagcctg tcaacttagg 1250
atggatggct gagagggctt cctaggagcc agtcacgcagg gtgggggtgg 1300
gccagaggag ctctccagcc ctgccttagt ggcgcctgta gccccttgc 1350
gtgtgctgag catggcatga ggctgaagt gcaaccctgg ggtctttgat 1400
gtcttgacag attgaccatc tgtctccagc caggccaccc ctttccaaaa 1450
ttccctcttc tgccagttact cccccctgtac cacccattgc tggcaca 1500
cccatcctta agctaagaca ggacgattgt ggtccctcca cactaaggcc 1550
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ctcctctggg agcatccatg tccccggagag ggtccctca acagtcagcc 1650

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<212> DNA

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<211> 201

<212> PRT

<213> Homo sapiens

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				20				25				30		

Thr	Glu	Pro	Ile	Val	Leu	Glu	Gly	Lys	Cys	Leu	Val	Val	Cys	Asp
					35			40				45		

Ser	Asn	Pro	Ala	Thr	Asp	Ser	Lys	Gly	Ser	Ser	Ser	Ser	Pro	Leu
				50				55				60		

Gly Ile Ser Val Arg Ala Ala Asn Ser Lys Val Ala Phe Ser Ala
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 Val Arg Ser Thr Asn His Glu Pro Ser Glu Met Ser Asn Lys Thr
 80 85 90
 Arg Ile Ile Tyr Phe Asp Gln Ile Leu Val Asn Val Gly Asn Phe
 95 100 105
 Phe Thr Leu Glu Ser Val Phe Val Ala Pro Arg Lys Gly Ile Tyr
 110 115 120
 Ser Phe Ser Phe His Val Ile Lys Val Tyr Gln Ser Gln Thr Ile
 125 130 135
 Gln Val Asn Leu Met Leu Asn Gly Lys Pro Val Ile Ser Ala Phe
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 Ala Gly Asp Lys Asp Val Thr Arg Glu Ala Ala Thr Asn Gly Val
 155 160 165
 Leu Leu Tyr Leu Asp Lys Glu Asp Lys Val Tyr Leu Lys Leu Glu
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 Phe Leu Val Phe Pro Leu
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 <223> Synthetic construct.

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 <213> Artificial

 <220>
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<212> DNA
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<212> DNA
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<210> 225
<211> 257
<212> PRT

<213> Homo sapiens

<400> 225

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Pro	Ala	Leu	Ala	Leu	Tyr	Val	Phe	Thr	Ile	Ala	Ile	Glu	Pro	Leu
				20					25					30
Arg	Ile	Ile	Phe	Leu	Ile	Ala	Gly	Ala	Phe	Phe	Trp	Leu	Val	Ser
				35					40					45
Leu	Leu	Ile	Ser	Ser	Leu	Val	Trp	Phe	Met	Ala	Arg	Val	Ile	Ile
				50					55					60
Asp	Asn	Lys	Asp	Gly	Pro	Thr	Gln	Lys	Tyr	Leu	Leu	Ile	Phe	Gly
				65					70					75
Ala	Phe	Val	Ser	Val	Tyr	Ile	Gln	Glu	Met	Phe	Arg	Phe	Ala	Tyr
				80					85					90
Tyr	Lys	Leu	Leu	Lys	Lys	Ala	Ser	Glu	Gly	Leu	Lys	Ser	Ile	Asn
				95					100					105
Pro	Gly	Glu	Thr	Ala	Pro	Ser	Met	Arg	Leu	Leu	Ala	Tyr	Val	Ser
				110					115					120
Gly	Leu	Gly	Phe	Gly	Ile	Met	Ser	Gly	Val	Phe	Ser	Phe	Val	Asn
				125					130					135
Thr	Leu	Ser	Asp	Ser	Leu	Gly	Pro	Gly	Thr	Val	Gly	Ile	His	Gly
				140					145					150
Asp	Ser	Pro	Gln	Phe	Phe	Leu	Tyr	Ser	Ala	Phe	Met	Thr	Leu	Val
				155					160					165
Ile	Ile	Leu	Leu	His	Val	Phe	Trp	Gly	Ile	Val	Phe	Phe	Asp	Gly
				170					175					180
Cys	Glu	Lys	Lys	Lys	Trp	Gly	Ile	Leu	Leu	Ile	Val	Leu	Leu	Thr
				185					190					195
His	Leu	Leu	Val	Ser	Ala	Gln	Thr	Phe	Ile	Ser	Ser	Tyr	Tyr	Gly
				200					205					210
Ile	Asn	Leu	Ala	Ser	Ala	Phe	Ile	Ile	Leu	Val	Leu	Met	Gly	Thr
				215					220					225
Trp	Ala	Phe	Leu	Ala	Ala	Gly	Gly	Ser	Cys	Arg	Ser	Leu	Lys	Leu
				230					235					240
Cys	Leu	Leu	Cys	Gln	Asp	Lys	Asn	Phe	Leu	Leu	Tyr	Asn	Gln	Arg
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<211> 3939
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20 25 30

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 35 40 45
 Glu Leu Val Asn Ile Tyr Thr Phe Asn His Thr Val Thr Arg Asn
 50 55 60
 Arg Thr Glu Gly Val Arg Val Ser Val Asn Val Leu Asn Lys Gln
 65 70 75
 Lys Gly Ala Pro Leu Leu Phe Val Val Arg Gln Lys Glu Ala Val
 80 85 90
 Val Ser Phe Gln Val Pro Leu Ile Leu Arg Gly Met Phe Gln Arg
 95 100 105
 Lys Tyr Leu Tyr Gln Lys Val Glu Arg Thr Leu Cys Gln Pro Pro
 110 115 120
 Thr Lys Asn Glu Ser Glu Ile Gln Phe Phe Tyr Val Asp Val Ser
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 140 145 150
 Met Asp Asp Phe Val Leu Arg Thr Gly Glu Gln Phe Ser Phe Asn
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 Thr Thr Ala Ala Gln Pro Gln Tyr Phe Lys Tyr Glu Phe Pro Glu
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 Gly Val Asp Ser Val Ile Val Lys Val Thr Ser Asn Lys Ala Phe
 185 190 195
 Pro Cys Ser Val Ile Ser Ile Gln Asp Val Leu Cys Pro Val Tyr
 200 205 210
 Asp Leu Asp Asn Asn Val Ala Phe Ile Gly Met Tyr Gln Thr Met
 215 220 225
 Thr Lys Lys Ala Ala Ile Thr Val Gln Arg Lys Asp Phe Pro Ser
 230 235 240
 Asn Ser Phe Tyr Val Val Val Val Lys Thr Glu Asp Gln Ala
 245 250 255
 Cys Gly Gly Ser Leu Pro Phe Tyr Pro Phe Ala Glu Asp Glu Pro
 260 265 270
 Val Asp Gln Gly His Arg Gln Lys Thr Leu Ser Val Leu Val Ser
 275 280 285
 Gln Ala Val Thr Ser Glu Ala Tyr Val Ser Gly Met Leu Phe Cys
 290 295 300
 Leu Gly Ile Phe Leu Ser Phe Tyr Leu Leu Thr Val Leu Leu Ala
 305 310 315
 Cys Trp Glu Asn Trp Arg Gln Lys Lys Lys Thr Leu Leu Val Ala

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335	340	345
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Ser Phe Glu Asn Val Ser Gly Ser Thr Asp	Gly Leu Val Asp Ser	
365	370	375
Ala Gly Thr Gly Asp Leu Ser Tyr Gly Tyr	Gln Gly Arg Ser Phe	
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Glu Pro Val Gly Thr Arg Pro Arg Val Asp	Ser Met Ser Ser Val	
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Glu Glu Asp Asp Tyr Asp Thr Leu Thr Asp	Ile Asp Ser Asp Lys	
410	415	420
Asn Val Ile Arg Thr Lys Gln Tyr Leu Tyr	Val Ala Asp Leu Ala	
425	430	435
Arg Lys Asp Lys Arg Val Leu Arg Lys Lys	Tyr Gln Ile Tyr Phe	
440	445	450
Trp Asn Ile Ala Thr Ile Ala Val Phe	Tyr Ala Leu Pro Val Val	
455	460	465
Gln Leu Val Ile Thr Tyr Gln Thr Val Val	Asn Val Thr Gly Asn	
470	475	480
Gln Asp Ile Cys Tyr Tyr Asn Phe Leu Cys	Ala His Pro Leu Gly	
485	490	495
Asn Leu Ser Ala Phe Asn Asn Ile Leu Ser	Asn Leu Gly Tyr Ile	
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Asn His Asn Arg Ala Leu Leu Arg Asn Asp	Leu Cys Ala Leu Glu	
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Cys Gly Ile Pro Lys His Phe Gly Leu Phe	Tyr Ala Met Gly Thr	
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Ala Leu Met Met Glu Gly Leu Leu Ser Ala	Cys Tyr His Val Cys	
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Pro Asn Tyr Thr Asn Phe Gln Phe Asp	Thr Ser Phe Met Tyr Met	
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Ile Ala Gly Leu Cys Met Leu Lys Leu Tyr	Gln Lys Arg His Pro	
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Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr	Ala Cys Leu Ala Ile	
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 Asp Ser Gly Ile Phe Arg Arg Ile Leu His Val Leu Tyr Thr Asp
 665 670 675
 Cys Ile Arg Gln Cys Ser Gly Pro Leu Tyr Val Asp Arg Met Val
 680 685 690
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 695 700 705
 Gly Leu Ile Met Arg Pro Asn Asp Phe Ala Ser Tyr Leu Leu Ala
 710 715 720
 Ile Gly Ile Cys Asn Leu Leu Leu Tyr Phe Ala Phe Tyr Ile Ile
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 Met Lys Leu Arg Ser Gly Glu Arg Ile Lys Leu Ile Pro Leu Leu
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 755 760 765
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 770 775 780
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caggtggacc ccacttcagg cagtgtgacg ctgggggtgc tcccactccg 1350
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<210> 229
<211> 807
<212> PRT
<213> Homo sapiens

<400> 229
Met Val Pro Ala Trp Leu Trp Leu Leu Cys Val Ser Val Pro Gln
1 5 10 15

Ala Leu Pro Lys Ala Gln Pro Ala Glu Leu Ser Val Glu Val Pro

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Glu Asn Tyr Gly Gly Asn Phe Pro Leu Tyr	Leu Thr Lys Leu Pro	
35	40	45
Leu Pro Arg Glu Gly Ala Glu Gly Gln Ile	Val Leu Ser Gly Asp	
50	55	60
Ser Gly Lys Ala Thr Glu Gly Pro Phe Ala	Met Asp Pro Asp Ser	
65	70	75
Gly Phe Leu Leu Val Thr Arg Ala Leu Asp	Arg Glu Glu Gln Ala	
80	85	90
Glu Tyr Gln Leu Gln Val Thr Leu Glu	Met Gln Asp Gly His Val	
95	100	105
Leu Trp Gly Pro Gln Pro Val Leu Val	His Val Lys Asp Glu Asn	
110	115	120
Asp Gln Val Pro His Phe Ser Gln Ala	Ile Tyr Arg Ala Arg Leu	
125	130	135
Ser Arg Gly Thr Arg Pro Gly Ile Pro	Phe Leu Phe Leu Glu Ala	
140	145	150
Ser Asp Arg Asp Glu Pro Gly Thr Ala	Asn Ser Asp Leu Arg Phe	
155	160	165
His Ile Leu Ser Gln Ala Pro Ala Gln	Pro Ser Pro Asp Met Phe	
170	175	180
Gln Leu Glu Pro Arg Leu Gly Ala Leu	Ala Leu Ser Pro Lys Gly	
185	190	195
Ser Thr Ser Leu Asp His Ala Leu Glu	Arg Thr Tyr Gln Leu Leu	
200	205	210
Val Gln Val Lys Asp Met Gly Asp Gln	Ala Ser Gly His Gln Ala	
215	220	225
Thr Ala Thr Val Glu Val Ser Ile Ile	Glu Ser Thr Trp Val Ser	
230	235	240
Leu Glu Pro Ile His Leu Ala Glu Asn	Leu Lys Val Leu Tyr Pro	
245	250	255
His His Met Ala Gln Val His Trp Ser	Gly Gly Asp Val His Tyr	
260	265	270
His Leu Glu Ser His Pro Pro Gly Pro	Phe Glu Val Asn Ala Glu	
275	280	285
Gly Asn Leu Tyr Val Thr Arg Glu Leu	Asp Arg Glu Ala Gln Ala	
290	295	300
Glu Tyr Leu Leu Gln Val Arg Ala Gln	Asn Ser His Gly Glu Asp	
305	310	315

Tyr Ala Ala Pro Leu Glu Leu His Val Leu Val Met Asp Glu Asn
 320 325 330
 Asp Asn Val Pro Ile Cys Pro Pro Arg Asp Pro Thr Val Ser Ile
 335 340 345
 Pro Glu Leu Ser Pro Pro Gly Thr Glu Val Thr Arg Leu Ser Ala
 350 355 360
 Glu Asp Ala Asp Ala Pro Gly Ser Pro Asn Ser His Val Val Tyr
 365 370 375
 Gln Leu Leu Ser Pro Glu Pro Glu Asp Gly Val Glu Gly Arg Ala
 380 385 390
 Phe Gln Val Asp Pro Thr Ser Gly Ser Val Thr Leu Gly Val Leu
 395 400 405
 Pro Leu Arg Ala Gly Gln Asn Ile Leu Leu Leu Val Leu Ala Met
 410 415 420
 Asp Leu Ala Gly Ala Glu Gly Phe Ser Ser Thr Cys Glu Val
 425 430 435
 Glu Val Ala Val Thr Asp Ile Asn Asp His Ala Pro Glu Phe Ile
 440 445 450
 Thr Ser Gln Ile Gly Pro Ile Ser Leu Pro Glu Asp Val Glu Pro
 455 460 465
 Gly Thr Leu Val Ala Met Leu Thr Ala Ile Asp Ala Asp Leu Glu
 470 475 480
 Pro Ala Phe Arg Leu Met Asp Phe Ala Ile Glu Arg Gly Asp Thr
 485 490 495
 Glu Gly Thr Phe Gly Leu Asp Trp Glu Pro Asp Ser Gly His Val
 500 505 510
 Arg Leu Arg Leu Cys Lys Asn Leu Ser Tyr Glu Ala Ala Pro Ser
 515 520 525
 His Glu Val Val Val Val Val Gln Ser Val Ala Lys Leu Val Gly
 530 535 540
 Pro Gly Pro Gly Pro Gly Ala Thr Ala Thr Val Thr Val Leu Val
 545 550 555
 Glu Arg Val Met Pro Pro Pro Lys Leu Asp Gln Glu Ser Tyr Glu
 560 565 570
 Ala Ser Val Pro Ile Ser Ala Pro Ala Gly Ser Phe Leu Leu Thr
 575 580 585
 Ile Gln Pro Ser Asp Pro Ile Ser Arg Thr Leu Arg Phe Ser Leu
 590 595 600
 Val Asn Asp Ser Glu Gly Trp Leu Cys Ile Glu Lys Phe Ser Gly

605	610	615
Glu Val His Thr Ala Gln Ser Leu Gln	Gly Ala Gln Pro Gly Asp	
620	625	630
Thr Tyr Thr Val Leu Val Glu Ala Gln Asp	Thr Ala Leu Thr Leu	
635	640	645
Ala Pro Val Pro Ser Gln Tyr Leu Cys	Thr Pro Arg Gln Asp His	
650	655	660
Gly Leu Ile Val Ser Gly Pro Ser Lys	Asp Pro Asp Leu Ala Ser	
665	670	675
Gly His Gly Pro Tyr Ser Phe Thr Leu	Gly Pro Asn Pro Thr Val	
680	685	690
Gln Arg Asp Trp Arg Leu Gln Thr Leu	Asn Gly Ser His Ala Tyr	
695	700	705
Leu Thr Leu Ala Leu His Trp Val Glu	Pro Arg Glu His Ile Ile	
710	715	720
Pro Val Val Val Ser His Asn Ala Gln	Met Trp Gln Leu Leu Val	
725	730	735
Arg Val Ile Val Cys Arg Cys Asn Val	Glu Gly Gln Cys Met Arg	
740	745	750
Lys Val Gly Arg Met Lys Gly Met Pro	Thr Lys Leu Ser Ala Val	
755	760	765
Gly Ile Leu Val Gly Thr Leu Val Ala	Ile Gly Ile Phe Leu Ile	
770	775	780
Leu Ile Phe Thr His Trp Thr Met Ser	Arg Lys Lys Asp Pro Asp	
785	790	795
Gln Pro Ala Asp Ser Val Pro Leu Lys	Ala Thr Val	
800	805	

<210> 230
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 230
cgccttaccg cgcaagccga agattcacta tggtaaaat cgccttcaat 50

<210> 231
<211> 24
<212> DNA
<213> Artificial Seqeunce

<220>
<221> Artificial Sequence
<222> full
<223> Synthetic oligonucleotide probe

<400> 231
cctgagctgt aaccccaactc cagg 24

<210> 232
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 232
agagtctgtc ccagctatct tgt 23

<210> 233
<211> 2786
<212> DNA
<213> Homo sapiens

<400> 233
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cagaaatgga gacgagatca gcaaatttgc tcaactatgt aattcaaaaca 150
acttgaagct caatttctgg aaatctccct cctcatttcaa tcggcctgtg 200
gatgtccctgg tcccatctgt cagttctgcag gcatttaaat ctttccttag 250
atcccagggc ttagagtgacg cagtgacaat tgaggacactg caggcccttt 300
tagacaatga agatgtatgaa atgcaacaca atgaaggcga agaacggagc 350
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cgagatggac aacattgccg cagactttcc tgacctggcg aggagggtga 450
agattggaca ttcttttggaa aaccggccga tgtatgtact gaagttcagc 500
actggaaag gcgtgaggcg gccggccgtt tggctgaatg caggcatcca 550
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atggatattt tcttgttgcc tgtggccaaat cctgtatggat atgtgtatac 700
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<210> 234

<211> 421

<212> PRT

<213> Homo sapiens

<400> 234

Met Arg Trp Ile Leu Phe Ile Gly Ala Leu Ile Gly Ser Ser Ile
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Cys Gly Gln Glu Lys Phe Phe Gly Asp Gln Val Leu Arg Ile Asn
20 25 30

Val Arg Asn Gly Asp Glu Ile Ser Lys Leu Ser Gln Leu Val Asn
35 40 45

Ser Asn Asn Leu Lys Leu Asn Phe Trp Lys Ser Pro Ser Ser Phe
50 55 60

Asn Arg Pro Val Asp Val Leu Val Pro Ser Val Ser Leu Gln Ala
65 70 75

Phe Lys Ser Phe Leu Arg Ser Gln Gly Leu Glu Tyr Ala Val Thr
80 85 90

Ile Glu Asp Leu Gln Ala Leu Leu Asp Asn Glu Asp Asp Glu Met
95 100 105

Gln His Asn Glu Gly Gln Glu Arg Ser Ser Asn Asn Phe Asn Tyr
110 115 120

Gly Ala Tyr His Ser Leu Glu Ala Ile Tyr His Glu Met Asp Asn
125 130 135

Ile Ala Ala Asp Phe Pro Asp Leu Ala Arg Arg Val Lys Ile Gly
140 145 150

His Ser Phe Glu Asn Arg Pro Met Tyr Val Leu Lys Phe Ser Thr
155 160 165

Gly Lys Gly Val Arg Arg Pro Ala Val Trp Leu Asn Ala Gly Ile
 170 175 180
 His Ser Arg Glu Trp Ile Ser Gln Ala Thr Ala Ile Trp Thr Ala
 185 190 195
 Arg Lys Ile Val Ser Asp Tyr Gln Arg Asp Pro Ala Ile Thr Ser
 200 205 210
 Ile Leu Glu Lys Met Asp Ile Phe Leu Leu Pro Val Ala Asn Pro
 215 220 225
 Asp Gly Tyr Val Tyr Thr Gln Thr Gln Asn Arg Leu Trp Arg Lys
 230 235 240
 Thr Arg Ser Arg Asn Pro Gly Ser Ser Cys Ile Gly Ala Asp Pro
 245 250 255
 Asn Arg Asn Trp Asn Ala Ser Phe Ala Gly Lys Gly Ala Ser Asp
 260 265 270
 Asn Pro Cys Ser Glu Val Tyr His Gly Pro His Ala Asn Ser Glu
 275 280 285
 Val Glu Val Lys Ser Val Val Asp Phe Ile Gln Lys His Gly Asn
 290 295 300
 Phe Lys Gly Phe Ile Asp Leu His Ser Tyr Ser Gln Leu Leu Met
 305 310 315
 Tyr Pro Tyr Gly Tyr Ser Val Lys Lys Ala Pro Asp Ala Glu Glu
 320 325 330
 Leu Asp Lys Val Ala Arg Leu Ala Ala Lys Ala Leu Ala Ser Val
 335 340 345
 Ser Gly Thr Glu Tyr Gln Val Gly Pro Thr Cys Thr Thr Val Tyr
 350 355 360
 Pro Ala Ser Gly Ser Ser Ile Asp Trp Ala Tyr Asp Asn Gly Ile
 365 370 375
 Lys Phe Ala Phe Thr Phe Glu Leu Arg Asp Thr Gly Thr Tyr Gly
 380 385 390
 Phe Leu Leu Pro Ala Asn Gln Ile Ile Pro Thr Ala Glu Glu Thr
 395 400 405
 Trp Leu Gly Leu Lys Thr Ile Met Glu His Val Arg Asp Asn Leu
 410 415 420

Tyr

<210> 235
 <211> 1743
 <212> DNA
 <213> Homo sapiens

<400> 235
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aacaccgact ttgccttccg cctataccgc aggctggttt tggagacccc 250
gagtcagaac atcttcttct cccctgtgag tgtctccact tccctggcca 300
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<210> 236

<211> 417

<212> PRT

<213> Homo sapiens

<400> 236

Met	Ala	Ser	Tyr	Leu	Tyr	Gly	Val	Leu	Phe	Ala	Val	Gly	Leu	Cys
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Ala	Pro	Ile	Tyr	Cys	Val	Ser	Pro	Ala	Asn	Ala	Pro	Ser	Ala	Tyr
	20					25							30	
Pro	Arg	Pro	Ser	Ser	Thr	Lys	Ser	Thr	Pro	Ala	Ser	Gln	Val	Tyr
	35					40							45	
Ser	Leu	Asn	Thr	Asp	Phe	Ala	Phe	Arg	Leu	Tyr	Arg	Arg	Leu	Val
	50					55							60	
Leu	Glu	Thr	Pro	Ser	Gln	Asn	Ile	Phe	Phe	Ser	Pro	Val	Ser	Val
	65					70							75	
Ser	Thr	Ser	Leu	Ala	Met	Leu	Ser	Leu	Gly	Ala	His	Ser	Val	Thr
	80					85							90	
Lys	Thr	Gln	Ile	Leu	Gln	Gly	Leu	Gly	Phe	Asn	Leu	Thr	His	Thr
	95					100							105	
Pro	Glu	Ser	Ala	Ile	His	Gln	Gly	Phe	Gln	His	Leu	Val	His	Ser
	110					115							120	
Leu	Thr	Val	Pro	Ser	Lys	Asp	Leu	Thr	Leu	Lys	Met	Gly	Ser	Ala
	125					130							135	
Leu	Phe	Val	Lys	Lys	Glu	Leu	Gln	Leu	Gln	Ala	Asn	Phe	Leu	Gly
	140					145							150	
Asn	Val	Lys	Arg	Leu	Tyr	Glu	Ala	Glu	Val	Phe	Ser	Thr	Asp	Phe
	155					160							165	
Ser	Asn	Pro	Ser	Ile	Ala	Gln	Ala	Arg	Ile	Asn	Ser	His	Val	Lys
	170					175							180	
Lys	Lys	Thr	Gln	Gly	Lys	Val	Val	Asp	Ile	Ile	Gln	Gly	Leu	Asp
	185					190							195	
Leu	Leu	Thr	Ala	Met	Val	Leu	Val	Asn	His	Ile	Phe	Phe	Lys	Ala

200	205	210
Lys Trp Glu Lys Pro Phe His Leu Glu Tyr Thr Arg Lys Asn Phe		
215	220	225
Pro Phe Leu Val Gly Glu Gln Val Thr Val Gln Val Pro Met Met		
230	235	240
His Gln Lys Glu Gln Phe Ala Phe Gly Val Asp Thr Glu Leu Asn		
245	250	255
Cys Phe Val Leu Gln Met Asp Tyr Lys Gly Asp Ala Val Ala Phe		
260	265	270
Phe Val Leu Pro Ser Lys Gly Lys Met Arg Gln Leu Glu Gln Ala		
275	280	285
Leu Ser Ala Arg Thr Leu Ile Lys Trp Ser His Ser Leu Gln Lys		
290	295	300
Arg Trp Ile Glu Val Phe Ile Pro Arg Phe Ser Ile Ser Ala Ser		
305	310	315
Tyr Asn Leu Glu Thr Ile Leu Pro Lys Met Gly Ile Gln Asn Ala		
320	325	330
Phe Asp Lys Asn Ala Asp Phe Ser Gly Ile Ala Lys Arg Asp Ser		
335	340	345
Leu Gln Val Ser Lys Ala Thr His Lys Ala Val Leu Asp Val Ser		
350	355	360
Glu Glu Gly Thr Glu Ala Thr Ala Ala Thr Thr Thr Lys Phe Ile		
365	370	375
Val Arg Ser Lys Asp Gly Pro Ser Tyr Phe Thr Val Ser Phe Asn		
380	385	390
Arg Thr Phe Leu Met Met Ile Thr Asn Lys Ala Thr Asp Gly Ile		
395	400	405
Leu Phe Leu Gly Lys Val Glu Asn Pro Thr Lys Ser		
410	415	

<210> 237

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 237

caaccatgca aggacagggc agg 23

<210> 238

<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 238
ctttgctgtt ggccctgtg ctcccaacca tgcaaggaca gggcagg 47

<210> 239
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 239
tgactcgaaa ctcctaaaaac cagc 24

<210> 240
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 240
ggtagatggcg gaaggcaaag tcgg 24

<210> 241
<211> 48
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-48
<223> Synthetic construct.

<400> 241
ggcatcttac ctttatggag tactcttgc tggcgttc tggcgtcc 48

<210> 242
<211> 2436
<212> DNA
<213> Homo sapiens

<400> 242
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<210> 243

<211> 596

<212> PRT

<213> Homo sapiens

<400> 243

Met	Lys	Met	Gln	Lys	Gly	Asn	Val	Leu	Leu	Met	Phe	Gly	Leu	Leu
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Leu	His	Leu	Glu	Ala	Ala	Thr	Asn	Ser	Asn	Glu	Thr	Ser	Thr	Ser
				20				25			30			
Ala	Asn	Thr	Gly	Ser	Ser	Val	Ile	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				35				40			45			
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Val	Ser	Thr	Ala
				50				55			60			
Thr	Ile	Ser	Gly	Ser	Ser	Val	Thr	Ser	Asn	Gly	Val	Ser	Ile	Val
				65				70			75			

Thr Asn Ser Glu Phe His Thr Thr Ser Ser Gly Ile Ser Thr Ala
 80 85 90

 Thr Asn Ser Glu Phe Ser Thr Ala Ser Ser Gly Ile Ser Ile Ala
 95 100 105

 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 110 115 120

 Thr Asn Ser Glu Ser Ser Thr Pro Ser Ser Gly Ala Ser Thr Val
 125 130 135

 Thr Asn Ser Gly Ser Ser Val Thr Ser Ser Gly Ala Ser Thr Ala
 140 145 150

 Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Arg Ala Ser Thr Ala
 155 160 165

 Thr Asn Ser Glu Ser Ser Thr Leu Ser Ser Gly Ala Ser Thr Ala
 170 175 180

 Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 185 190 195

 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 200 205 210

 Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Arg Ala Ser Thr Ala
 215 220 225

 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 230 235 240

 Thr Asn Ser Glu Ser Arg Thr Thr Ser Asn Gly Ala Gly Thr Ala
 245 250 255

 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 260 265 270

 Thr Asn Ser Asp Ser Ser Thr Val Ser Ser Gly Ala Ser Thr Ala
 275 280 285

 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 290 295 300

 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 305 310 315

 Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Gly Ala Gly Thr Ala
 320 325 330

 Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ile Ser Thr Val
 335 340 345

 Thr Asn Ser Glu Ser Ser Thr Pro Ser Ser Gly Ala Asn Thr Ala
 350 355 360

 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Asn Thr Ala

365	370	375
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ala Ser Thr Ala		
380	385	390
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Val Ser Thr Ala		
395	400	405
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala		
410	415	420
Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala		
425	430	435
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ile Ser Thr Val		
440	445	450
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Asn Thr Ala		
455	460	465
Thr Asn Ser Gly Ser Ser Val Thr Ser Ala Gly Ser Gly Thr Ala		
470	475	480
Ala Leu Thr Gly Met His Thr Thr Ser His Ser Ala Ser Thr Ala		
485	490	495
Val Ser Glu Ala Lys Pro Gly Gly Ser Leu Val Pro Trp Glu Ile		
500	505	510
Phe Leu Ile Thr Leu Val Ser Val Val Ala Ala Val Gly Leu Phe		
515	520	525
Ala Gly Leu Phe Phe Cys Val Arg Asn Ser Leu Ser Leu Arg Asn		
530	535	540
Thr Phe Asn Thr Ala Val Tyr His Pro His Gly Leu Asn His Gly		
545	550	555
Leu Gly Pro Gly Pro Gly Gly Asn His Gly Ala Pro His Arg Pro		
560	565	570
Arg Trp Ser Pro Asn Trp Phe Trp Arg Arg Pro Val Ser Ser Ile		
575	580	585
Ala Met Glu Met Ser Gly Arg Asn Ser Gly Pro		
590	595	
<210> 244		
<211> 26		
<212> DNA		
<213> Artificial		
<220>		
<221> Artificial Sequence		
<222> 1-26		
<223> Synthetic construct.		
<400> 244		

gaagcaccag cctttatctc ttcacc 26
<210> 245
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic sequence.

<400> 245
gtcagagttg gtggctgtgc tagc 24

<210> 246
<211> 48
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-48
<223> Synthetic construct.

<400> 246
ggacccaggc atcttgcttt ccagccacaa agagacagat gaagatgc 48

<210> 247
<211> 957
<212> DNA
<213> Homo sapiens

<400> 247
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tccctcccttc tgctactggg ggcctgtct ggatgggcgg ccagcgatga 150
ccccattttag aaggtcattt aaggatcaa ccgagggctg agcaatgcag 200
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gttgtcaat cagctgacat gacctggagg gttgggggt gggggacagg 900
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tacacca 957

<210> 248

<211> 247

<212> PRT

<213> Homo sapiens

<400> 248

Met His Leu Ala Arg Leu Val Gly Ser Cys Ser Leu Leu Leu
1 5 10 15

Leu Gly Ala Leu Ser Gly Trp Ala Ala Ser Asp Asp Pro Ile Glu
20 25 30

Lys Val Ile Glu Gly Ile Asn Arg Gly Leu Ser Asn Ala Glu Arg
35 40 45

Glu Val Gly Lys Ala Leu Asp Gly Ile Asn Ser Gly Ile Thr His
50 55 60

Ala Gly Arg Glu Val Glu Lys Val Phe Asn Gly Leu Ser Asn Met
65 70 75

Gly Ser His Thr Gly Lys Glu Leu Asp Lys Gly Val Gln Gly Leu
80 85 90

Asn His Gly Met Asp Lys Val Ala His Glu Ile Asn His Gly Ile
95 100 105

Gly Gln Ala Gly Lys Glu Ala Glu Lys Leu Gly His Gly Val Asn
110 115 120

Asn Ala Ala Gly Gln Ala Gly Lys Glu Ala Asp Lys Ala Val Gln
125 130 135

Gly Phe His Thr Gly Val His Gln Ala Gly Lys Glu Ala Glu Lys
140 145 150

Leu Gly Gln Gly Val Asn His Ala Ala Asp Gln Ala Gly Lys Glu
155 160 165

Val Glu Lys Leu Gly Gln Gly Ala His His Ala Ala Gly Gln Ala
170 175 180

Gly Lys Glu Leu Gln Asn Ala His Asn Gly Val Asn Gln Ala Ser
185 190 195

Lys Glu Ala Asn Gln Leu Leu Asn Gly Asn His Gln Ser Gly Ser
200 205 210

Ser Ser His Gln Gly Gly Ala Thr Thr Pro Leu Ala Ser Gly
215 220 225

Ala Ser Val Asn Thr Pro Phe Ile Asn Leu Pro Ala Leu Trp Arg
230 235 240

Ser Val Ala Asn Ile Met Pro
245

<210> 249
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 249
caatatgcatttgcacgtc tgg 23

<210> 250
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 250
aagcttccttgcatttttc ctgc 24

<210> 251
<211> 43
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-43
<223> Synthetic construct.

<400> 251
tgacccttgcatttgcatttttc ttgaaggat caaccgaggg ctg 43

<210> 252
<211> 3781
<212> DNA
<213> Homo sapiens

<400> 252
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<210> 253

<211> 837

<212> PRT

<213> Homo sapiens

<400> 253

Met	Leu	Arg	Thr	Ala	Met	Gly	Leu	Arg	Ser	Trp	Leu	Ala	Ala	Pro
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Trp	Gly	Ala	Leu	Pro	Pro	Arg	Pro	Pro	Leu	Leu	Leu	Leu	Leu	Leu
				20					25					30

Leu	Leu	Leu	Leu	Leu	Gln	Pro	Pro	Pro	Pro	Thr	Trp	Ala	Leu	Ser
					35					40				45

Pro	Arg	Ile	Ser	Leu	Pro	Leu	Gly	Ser	Glu	Glu	Arg	Pro	Phe	Leu
				50				55						60

Arg	Phe	Glu	Ala	Glu	His	Ile	Ser	Asn	Tyr	Thr	Ala	Leu	Leu	Leu
					65				70					75

Ser Arg Asp Gly Arg Thr Leu Tyr Val Gly Ala Arg Glu Ala Leu

80	85	90
Phe Ala Leu Ser Ser Asn Leu Ser Phe	Leu Pro Gly Gly Glu	Tyr
95	100	105
Gln Glu Leu Leu Trp Gly Ala Asp Ala	Glu Lys Lys Gln Gln Cys	
110	115	120
Ser Phe Lys Gly Lys Asp Pro Gln Arg Asp	Cys Gln Asn Tyr Ile	
125	130	135
Lys Ile Leu Leu Pro Leu Ser Gly Ser His	Leu Phe Thr Cys Gly	
140	145	150
Thr Ala Ala Phe Ser Pro Met Cys Thr Tyr	Ile Asn Met Glu Asn	
155	160	165
Phe Thr Leu Ala Arg Asp Glu Lys Gly Asn	Val Leu Leu Glu Asp	
170	175	180
Gly Lys Gly Arg Cys Pro Phe Asp Pro Asn	Phe Lys Ser Thr Ala	
185	190	195
Leu Val Val Asp Gly Glu Leu Tyr Thr	Gly Thr Val Ser Ser Phe	
200	205	210
Gln Gly Asn Asp Pro Ala Ile Ser Arg Ser	Gln Ser Leu Arg Pro	
215	220	225
Thr Lys Thr Glu Ser Ser Leu Asn Trp	Leu Gln Asp Pro Ala Phe	
230	235	240
Val Ala Ser Ala Tyr Ile Pro Glu Ser	Leu Gly Ser Leu Gln Gly	
245	250	255
Asp Asp Asp Lys Ile Tyr Phe Phe Ser	Glu Thr Gly Gln Glu	
260	265	270
Phe Glu Phe Phe Glu Asn Thr Ile Val Ser	Arg Ile Ala Arg Ile	
275	280	285
Cys Lys Gly Asp Glu Gly Glu Arg Val	Leu Gln Gln Arg Trp	
290	295	300
Thr Ser Phe Leu Lys Ala Gln Leu Leu	Cys Ser Arg Pro Asp Asp	
305	310	315
Gly Phe Pro Phe Asn Val Leu Gln Asp	Val Phe Thr Leu Ser Pro	
320	325	330
Ser Pro Gln Asp Trp Arg Asp Thr Leu	Phe Tyr Gly Val Phe Thr	
335	340	345
Ser Gln Trp His Arg Gly Thr Thr Glu	Gly Ser Ala Val Cys Val	
350	355	360
Phe Thr Met Lys Asp Val Gln Arg Val	Phe Ser Gly Leu Tyr Lys	
365	370	375

Glu Val Asn Arg Glu Thr Gln Gln Trp Tyr Thr Val Thr His Pro
 380 385 390
 Val Pro Thr Pro Arg Pro Gly Ala Cys Ile Thr Asn Ser Ala Arg
 395 400 405
 Glu Arg Lys Ile Asn Ser Ser Leu Gln Leu Pro Asp Arg Val Leu
 410 415 420
 Asn Phe Leu Lys Asp His Phe Leu Met Asp Gly Gln Val Arg Ser
 425 430 435
 Arg Met Leu Leu Leu Gln Pro Gln Ala Arg Tyr Gln Arg Val Ala
 440 445 450
 Val His Arg Val Pro Gly Leu His His Thr Tyr Asp Val Leu Phe
 455 460 465
 Leu Gly Thr Gly Asp Gly Arg Leu His Lys Ala Val Ser Val Gly
 470 475 480
 Pro Arg Val His Ile Ile Glu Glu Leu Gln Ile Phe Ser Ser Gly
 485 490 495
 Gln Pro Val Gln Asn Leu Leu Leu Asp Thr His Arg Gly Leu Leu
 500 505 510
 Tyr Ala Ala Ser His Ser Gly Val Val Gln Val Pro Met Ala Asn
 515 520 525
 Cys Ser Leu Tyr Arg Ser Cys Gly Asp Cys Leu Leu Ala Arg Asp
 530 535 540
 Pro Tyr Cys Ala Trp Ser Gly Ser Ser Cys Lys His Val Ser Leu
 545 550 555
 Tyr Gln Pro Gln Leu Ala Thr Arg Pro Trp Ile Gln Asp Ile Glu
 560 565 570
 Gly Ala Ser Ala Lys Asp Leu Cys Ser Ala Ser Ser Val Val Ser
 575 580 585
 Pro Ser Phe Val Pro Thr Gly Glu Lys Pro Cys Glu Gln Val Gln
 590 595 600
 Phe Gln Pro Asn Thr Val Asn Thr Leu Ala Cys Pro Leu Leu Ser
 605 610 615
 Asn Leu Ala Thr Arg Leu Trp Leu Arg Asn Gly Ala Pro Val Asn
 620 625 630
 Ala Ser Ala Ser Cys His Val Leu Pro Thr Gly Asp Leu Leu Leu
 635 640 645
 Val Gly Thr Gln Gln Leu Gly Glu Phe Gln Cys Trp Ser Leu Glu
 650 655 660
 Glu Gly Phe Gln Gln Leu Val Ala Ser Tyr Cys Pro Glu Val Val

665	670	675
Glu Asp Gly Val Ala Asp Gln Thr Asp	Glu Gly Gly Ser Val Pro	
680	685	690
Val Ile Ile Ser Thr Ser Arg Val Ser Ala Pro Ala Gly Gly Lys		
695	700	705
Ala Ser Trp Gly Ala Asp Arg Ser Tyr	Trp Lys Glu Phe Leu Val	
710	715	720
Met Cys Thr Leu Phe Val Leu Ala Val	Leu Leu Pro Val Leu Phe	
725	730	735
Leu Leu Tyr Arg His Arg Asn Ser Met	Lys Val Phe Leu Lys Gln	
740	745	750
Gly Glu Cys Ala Ser Val His Pro Lys	Thr Cys Pro Val Val Leu	
755	760	765
Pro Pro Glu Thr Arg Pro Leu Asn Gly	Leu Gly Pro Pro Ser Thr	
770	775	780
Pro Leu Asp His Arg Gly Tyr Gln Ser	Leu Ser Asp Ser Pro Pro	
785	790	795
Gly Ala Arg Val Phe Thr Glu Ser Glu	Lys Arg Pro Leu Ser Ile	
800	805	810
Gln Asp Ser Phe Val Glu Val Ser Pro	Val Cys Pro Arg Pro Arg	
815	820	825
Val Arg Leu Gly Ser Glu Ile Arg Asp	Ser Val Val	
830	835	

<210> 254
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 254
agccccgtgca gaatctgctc ctgg 24

<210> 255
<211> 24
<212> DNA
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<220>
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<222> 1-24
<223> Synthetic construct.

<400> 255
tgaagccagg gcagcgtcct ctgg 24

<210> 256
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<223> Synthetic construct.

<400> 256
gtacaggctg cagttggc 18

<210> 257
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<222> 1-41
<223> Synthetic construct.

<400> 257
agaagccatg tgagcaagtc cagttccagc ccaacacagt g 41

<210> 258
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<213> Artificial

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<222> 1-45
<223> Synthetic construct.

<400> 258
gagctgcaga tcttctcatc gggacagccc gtgcagaatc tgctc 45

<210> 259
<211> 4563
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 3635
<223> unknown base

<400> 259
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tgccggcccc gcgtccccgc gcgcgagcgg gaggagccgc cgccacctcg 200
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caggccgcgg cggcgggggc gggtgtgcgg aacaaggcg cggcgcgggg 300
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tgggcggggg cagcgggctg agggcgcgcg gagcctgcgg cggcggcg 450
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<210> 260
 <211> 802
 <212> PRT
 <213> Homo sapiens

<400> 260
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Leu Val Leu Gly Phe Val Leu Ala Ser Arg Leu Val Leu Pro Arg
 20 25 30

Ala Ser Glu Leu Lys Arg Ala Gly Pro Arg Arg Arg Ala Ser Pro
 35 40 45

Glu Gly Cys Arg Ser Gly Gln Ala Ala Ala Ser Gln Ala Gly Gly
 50 55 60

Ala Arg Gly Asp Ala Arg Gly Ala Gln Leu Trp Pro Pro Gly Ser
 65 70 75

Asp Pro Asp Gly Gly Pro Arg Asp Arg Asn Phe Leu Phe Val Gly
 80 85 90

Val Met Thr Ala Gln Lys Tyr Leu Gln Thr Arg Ala Val Ala Ala
 95 100 105

Tyr Arg Thr Trp Ser Lys Thr Ile Pro Gly Lys Val Gln Phe Phe
 110 115 120

Ser Ser Glu Gly Ser Asp Thr Ser Val Pro Ile Pro Val Val Pro
 125 130 135

Leu Arg Gly Val Asp Asp Ser Tyr Pro Pro Gln Lys Lys Ser Phe
 140 145 150

Met Met Leu Lys Tyr Met His Asp His Tyr Leu Asp Lys Tyr Glu
 155 160 165

Trp Phe Met Arg Ala Asp Asp Asp Val Tyr Ile Lys Gly Asp Arg
 170 175 180

Leu Glu Asn Phe Leu Arg Ser Leu Asn Ser Ser Glu Pro Leu Phe
 185 190 195

Leu Gly Gln Thr Gly Leu Gly Thr Thr Glu Glu Met Gly Lys Leu
 200 205 210

Ala Leu Glu Pro Gly Glu Asn Phe Cys Met Gly Gly Pro Gly Val
 215 220 225

Ile Met Ser Arg Glu Val Leu Arg Arg Met Val Pro His Ile Gly
 230 235 240

Lys Cys Leu Arg Glu Met Tyr Thr Thr His Glu Asp Val Glu Val
 245 250 255
 Gly Arg Cys Val Arg Arg Phe Ala Gly Val Gln Cys Val Trp Ser
 260 265 270
 Tyr Glu Met Arg Gln Leu Phe Tyr Glu Asn Tyr Glu Gln Asn Lys
 275 280 285
 Lys Gly Tyr Ile Arg Asp Leu His Asn Ser Lys Ile His Gln Ala
 290 295 300
 Ile Thr Leu His Pro Asn Lys Asn Pro Pro Tyr Gln Tyr Arg Leu
 305 310 315
 His Ser Tyr Met Leu Ser Arg Lys Ile Ser Glu Leu Arg His Arg
 320 325 330
 Thr Ile Gln Leu His Arg Glu Ile Val Leu Met Ser Lys Tyr Ser
 335 340 345
 Asn Thr Glu Ile His Lys Glu Asp Leu Gln Leu Gly Ile Pro Pro
 350 355 360
 Ser Phe Met Arg Phe Gln Pro Arg Gln Arg Glu Glu Ile Leu Glu
 365 370 375
 Trp Glu Phe Leu Thr Gly Lys Tyr Leu Tyr Ser Ala Val Asp Gly
 380 385 390
 Gln Pro Pro Arg Arg Gly Met Asp Ser Ala Gln Arg Glu Ala Leu
 395 400 405
 Asp Asp Ile Val Met Gln Val Met Glu Met Ile Asn Ala Asn Ala
 410 415 420
 Lys Thr Arg Gly Arg Ile Ile Asp Phe Lys Glu Ile Gln Tyr Gly
 425 430 435
 Tyr Arg Arg Val Asn Pro Met Tyr Gly Ala Glu Tyr Ile Leu Asp
 440 445 450
 Leu Leu Leu Tyr Lys Lys His Lys Gly Lys Lys Met Thr Val
 455 460 465
 Pro Val Arg Arg His Ala Tyr Leu Gln Gln Thr Phe Ser Lys Ile
 470 475 480
 Gln Phe Val Glu His Glu Glu Leu Asp Ala Gln Glu Leu Ala Lys
 485 490 495
 Arg Ile Asn Gln Glu Ser Gly Ser Leu Ser Phe Leu Ser Asn Ser
 500 505 510
 Leu Lys Lys Leu Val Pro Phe Gln Leu Pro Gly Ser Lys Ser Glu
 515 520 525
 His Lys Glu Pro Lys Asp Lys Lys Ile Asn Ile Leu Ile Pro Leu

530	535	540
Ser Gly Arg Phe Asp Met Phe Val Arg	Phe Met Gly Asn Phe	Glu
545	550	555
Lys Thr Cys Leu Ile Pro Asn Gln Asn	Val Lys Leu Val Val	Leu
560	565	570
Leu Phe Asn Ser Asp Ser Asn Pro Asp	Lys Ala Lys Gln Val	Glu
575	580	585
Leu Met Arg Asp Tyr Arg Ile Lys Tyr	Pro Lys Ala Asp Met	Gln
590	595	600
Ile Leu Pro Val Ser Gly Glu Phe Ser	Arg Ala Leu Ala Leu	Glu
605	610	615
Val Gly Ser Ser Gln Phe Asn Asn Glu	Ser Leu Leu Phe Phe	Cys
620	625	630
Asp Val Asp Leu Val Phe Thr Thr Glu	Phe Leu Gln Arg Cys	Arg
635	640	645
Ala Asn Thr Val Leu Gly Gln Gln	Ile Tyr Phe Pro Ile Ile	Phe
650	655	660
Ser Gln Tyr Asp Pro Lys Ile Val Tyr	Ser Gly Lys Val Pro	Ser
665	670	675
Asp Asn His Phe Ala Phe Thr Gln Lys	Thr Gly Phe Trp Arg	Asn
680	685	690
Tyr Gly Phe Gly Ile Thr Cys Ile Tyr	Lys Gly Asp Leu Val	Arg
695	700	705
Val Gly Gly Phe Asp Val Ser Ile Gln	Gly Trp Gly Leu Glu	Asp
710	715	720
Val Asp Leu Phe Asn Lys Val Val Gln	Ala Gly Leu Lys Thr	Phe
725	730	735
Arg Ser Gln Glu Val Gly Val Val His	Val His His Pro Val	Phe
740	745	750
Cys Asp Pro Asn Leu Asp Pro Lys Gln	Tyr Lys Met Cys Leu	Gly
755	760	765
Ser Lys Ala Ser Thr Tyr Gly Ser Thr	Gln Gln Leu Ala Glu	Met
770	775	780
Trp Leu Glu Lys Asn Asp Pro Ser Tyr	Ser Lys Ser Ser Asn	Asn
785	790	795
Asn Gly Ser Val Arg Thr Ala		
800		

<210> 261
<211> 24

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 261
gtgccactac ggggtgtgga cgac 24

<210> 262
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 262
tcccatttct tccgtggc ccag 24

<210> 263
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 263
ccagaagaag tccttcatga tgctcaagta catgcacgac cactac 46

<210> 264
<211> 1419
<212> DNA
<213> Homo sapiens

<400> 264
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tgacacccttc ctttcggcc ttgagggttcc cagcctggc gccccaggac 100
gttccggctcg catggcagag tgctacggac gacgcctatg aagcccttag 150
tccttctagt tgcgttttg ctatggcctt cgtctgtgcc ggcttatccg 200
agcataactg tgacacccctga tgaagagcaa aacttgaatc attatataca 250
agtttttagag aaccttagtac gaagtgttcc ctctggggag ccaggtcgtg 300
agaaaaaaatc taactctcca aaacatgttt attctatagc atcaaaggaa 350
tcaaaaattta aggagctagt tacacatgga gacgcttcaa ctgagaatga 400

tgttttaacc aatccttatca gtgaagaaaac tacaacttgc cctacaggag 450
gcttcacacc ggaaatagga aagaaaaaac acacggaaag taccccatc 500
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attttggttc aggaaaaaaa 1419

<210> 265

<211> 350

<212> PRT

<213> Homo sapiens

<400> 265

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Ser	Val	Pro	Ala	Tyr	Pro	Ser	Ile	Thr	Val	Thr	Pro	Asp	Glu	Glu
														30

Gln	Asn	Leu	Asn	His	Tyr	Ile	Gln	Val	Leu	Glu	Asn	Leu	Val	Arg
														45

Ser Val Pro Ser Gly Glu Pro Gly Arg Glu Lys Lys Ser Asn Ser

50	55	60
Pro Lys His Val Tyr Ser Ile Ala Ser Lys Gly Ser Lys Phe Lys		
65	70	75
Glu Leu Val Thr His Gly Asp Ala Ser Thr Glu Asn Asp Val Leu		
80	85	90
Thr Asn Pro Ile Ser Glu Glu Thr Thr Phe Pro Thr Gly Gly		
95	100	105
Phe Thr Pro Glu Ile Gly Lys Lys His Thr Glu Ser Thr Pro		
110	115	120
Phe Trp Ser Ile Lys Pro Asn Asn Val Ser Ile Val Leu His Ala		
125	130	135
Glu Glu Pro Tyr Ile Glu Asn Glu Glu Pro Glu Pro Glu Pro Glu		
140	145	150
Pro Ala Ala Lys Gln Thr Glu Ala Pro Arg Met Leu Pro Val Val		
155	160	165
Thr Glu Ser Ser Thr Ser Pro Tyr Val Thr Ser Tyr Lys Ser Pro		
170	175	180
Val Thr Thr Leu Asp Lys Ser Thr Gly Ile Glu Ile Ser Thr Glu		
185	190	195
Ser Glu Asp Val Pro Gln Leu Ser Gly Glu Thr Ala Ile Glu Lys		
200	205	210
Pro Glu Glu Phe Gly Lys His Pro Glu Ser Trp Asn Asn Asp Asp		
215	220	225
Ile Leu Lys Lys Ile Leu Asp Ile Asn Ser Gln Val Gln Gln Ala		
230	235	240
Leu Leu Ser Asp Thr Ser Asn Pro Ala Tyr Arg Glu Asp Ile Glu		
245	250	255
Ala Ser Lys Asp His Leu Lys Arg Ser Leu Ala Leu Ala Ala Ala		
260	265	270
Ala Glu His Lys Leu Lys Thr Met Tyr Lys Ser Gln Leu Leu Pro		
275	280	285
Val Gly Arg Thr Ser Asn Lys Ile Asp Asp Ile Glu Thr Val Ile		
290	295	300
Asn Met Leu Cys Asn Ser Arg Ser Lys Leu Tyr Glu Tyr Leu Asp		
305	310	315
Ile Lys Cys Val Pro Pro Glu Met Arg Glu Lys Ala Ala Thr Val		
320	325	330
Phe Asn Thr Leu Lys Asn Met Cys Arg Ser Arg Arg Val Thr Ala		
335	340	345

Leu Leu Lys Val Tyr
350

<210> 266

<211> 2403

<212> DNA

<213> Homo sapiens

<400> 266

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ttcatatgtt gagatcaacc cacaggaata tccatggctt ttgtgctcat 150

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gaccgggcaa gtttgtccag gccttggtgg gggaggacgc cgtgttctcc 250

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gaaagcacgg acaggcagaa ttgagagacg cccgaaaca cgcagtggag 1000

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gaaaactgtt acccatagaa aagctccccaa ggaggtgcct cactctgaga 1100

agagatttac aaggaagagt gtggtggctt ctcagggttt ccaaggcagg 1150

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tgAGGGCACA GTGTTGCTA ATGATGTGTT tttatTTTACATTTCCC 2000
accATAAAACT CTGTTGCTT ATTCCACATT AATTACTTT TCTCTATAACC 2050
aaATCACCCA TGGAAATAGTT ATTGAACACC TGCTTGTA ggCTCAAAGA 2100
ataAAAGAGGA GGTAGGATTt TTCACTGATT CTATAAGCCC AGCATTACCT 2150
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caaATTAAC TAAACAATAT ATTAAAGAT GATATATAAC TACTCAGTGT 2300
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gtaATTCAgC ACATTAATAA AGTAAAAAAAG AAAACCATAA AAAAAAAAGA 2400
aaa 2403

<210> 267
<211> 466
<212> PRT
<213> Homo sapiens

<400> 267
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Ser Gly Gln Trp Gln Val Thr Gly Pro Gly Lys Phe Val Gln Ala

20	25	30
Leu Val Gly Glu Asp Ala Val Phe Ser Cys Ser Leu Phe Pro Glu		
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Thr Ser Ala Glu Ala Met Glu Val Arg Phe Phe Arg Asn Gln Phe		
50	55	60
His Ala Val Val His Leu Tyr Arg Asp Gly Glu Asp Trp Glu Ser		
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Lys Gln Met Pro Gln Tyr Arg Gly Arg Thr Glu Phe Val Lys Asp		
80	85	90
Ser Ile Ala Gly Gly Arg Val Ser Leu Arg Leu Lys Asn Ile Thr		
95	100	105
Pro Ser Asp Ile Gly Leu Tyr Gly Cys Trp Phe Ser Ser Gln Ile		
110	115	120
Tyr Asp Glu Glu Ala Thr Trp Glu Leu Arg Val Ala Ala Leu Gly		
125	130	135
Ser Leu Pro Leu Ile Ser Ile Val Gly Tyr Val Asp Gly Gly Ile		
140	145	150
Gln Leu Leu Cys Leu Ser Ser Gly Trp Phe Pro Gln Pro Thr Ala		
155	160	165
Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Ser Asp Ser Arg		
170	175	180
Ala Asn Ala Asp Gly Tyr Ser Leu Tyr Asp Val Glu Ile Ser Ile		
185	190	195
Ile Val Gln Glu Asn Ala Gly Ser Ile Leu Cys Ser Ile His Leu		
200	205	210
Ala Glu Gln Ser His Glu Val Glu Ser Lys Val Leu Ile Gly Glu		
215	220	225
Thr Phe Phe Gln Pro Ser Pro Trp Arg Leu Ala Ser Ile Leu Leu		
230	235	240
Gly Leu Leu Cys Gly Ala Leu Cys Gly Val Val Met Gly Met Ile		
245	250	255
Ile Val Phe Phe Lys Ser Lys Gly Lys Ile Gln Ala Glu Leu Asp		
260	265	270
Trp Arg Arg Lys His Gly Gln Ala Glu Leu Arg Asp Ala Arg Lys		
275	280	285
His Ala Val Glu Val Thr Leu Asp Pro Glu Thr Ala His Pro Lys		
290	295	300
Leu Cys Val Ser Asp Leu Lys Thr Val Thr His Arg Lys Ala Pro		
305	310	315

Gln Glu Val Pro His Ser Glu Lys Arg Phe Thr Arg Lys Ser Val
320 325 330

Val Ala Ser Gln Gly Phe Gln Ala Gly Arg His Tyr Trp Glu Val
335 340 345

Asp Val Gly Gln Asn Val Gly Trp Tyr Val Gly Val Cys Arg Asp
350 355 360

Asp Val Asp Arg Gly Lys Asn Asn Val Thr Leu Ser Pro Asn Asn
365 370 375

Gly Tyr Trp Val Leu Arg Leu Thr Thr Glu His Leu Tyr Phe Thr
380 385 390

Phe Asn Pro His Phe Ile Ser Leu Pro Pro Ser Thr Pro Pro Thr
395 400 405

Arg Val Gly Val Phe Leu Asp Tyr Glu Gly Gly Thr Ile Ser Phe
410 415 420

Phe Asn Thr Asn Asp Gln Ser Leu Ile Tyr Thr Leu Leu Thr Cys
425 430 435

Gln Phe Glu Gly Leu Leu Arg Pro Tyr Ile Gln His Ala Met Tyr
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Asp Glu Glu Lys Gly Thr Pro Ile Phe Ile Cys Pro Val Ser Trp
455 460 465

Gly

<210> 268
<211> 2103
<212> DNA
<213> Homo sapiens

<400> 268
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agttcagtca acagaagcat ggagtgttgg ctcatatgct gttgatttgt 400
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caggatcgTT ggtgggACAG aagtAAGAAGA gggtGAATGG ccctGGCAGG 650
ctAGCCTGCA gtgggatGGG agtcatcgCT gtggAGCAAC cttaATTAA 700
gccACATGGC ttgtgAGTGC tgctcACTGT tttACAACAT ataAGAACCC 750
tgCCAGATGG actgcttcCT ttggAGTAAC aataAAACCT tcgAAAATGA 800
aacggggTCT ccggAGAATA attgtccATG AAAAATACAA acACCCATCA 850
catgactATG atatttCTCT tgcAGAGCT tctAGCCCTG ttCCCTACAC 900
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caggTgATGT gATTTGtg acaggATTG gagcACTGAA aaATgATGGT 1000
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cca 2103
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<211> 423
<212> PRT
<213> Homo sapiens
<400> 269
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35 40 45
Asn Gln Lys Lys Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr
50 55 60
Thr Asp Lys Leu Tyr Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn
65 70 75
Phe Thr Glu Met Ser Gln Arg Leu Glu Ser Met Val Lys Asn Ala
80 85 90
Phe Tyr Lys Ser Pro Leu Arg Glu Glu Phe Val Lys Ser Gln Val
95 100 105
Ile Lys Phe Ser Gln Gln Lys His Gly Val Leu Ala His Met Leu
110 115 120
Leu Ile Cys Arg Phe His Ser Thr Glu Asp Pro Glu Thr Val Asp
125 130 135
Lys Ile Val Gln Leu Val Leu His Glu Lys Leu Gln Asp Ala Val
140 145 150
Gly Pro Pro Lys Val Asp Pro His Ser Val Lys Ile Lys Lys Ile
155 160 165
Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys Cys Gly Thr
170 175 180
Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val Gly Gly
185 190 195
Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln
200 205 210
Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile Asn Ala Thr
215 220 225

Trp Leu Val Ser Ala Ala His Cys Phe Thr Thr Tyr Lys Asn Pro
 230 235 240
 Ala Arg Trp Thr Ala Ser Phe Gly Val Thr Ile Lys Pro Ser Lys
 245 250 255
 Met Lys Arg Gly Leu Arg Arg Ile Ile Val His Glu Lys Tyr Lys
 260 265 270
 His Pro Ser His Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser
 275 280 285
 Pro Val Pro Tyr Thr Asn Ala Val His Arg Val Cys Leu Pro Asp
 290 295 300
 Ala Ser Tyr Glu Phe Gln Pro Gly Asp Val Met Phe Val Thr Gly
 305 310 315
 Phe Gly Ala Leu Lys Asn Asp Gly Tyr Ser Gln Asn His Leu Arg
 320 325 330
 Gln Ala Gln Val Thr Leu Ile Asp Ala Thr Thr Cys Asn Glu Pro
 335 340 345
 Gln Ala Tyr Asn Asp Ala Ile Thr Pro Arg Met Leu Cys Ala Gly
 350 355 360
 Ser Leu Glu Gly Lys Thr Asp Ala Cys Gln Gly Asp Ser Gly Gly
 365 370 375
 Pro Leu Val Ser Ser Asp Ala Arg Asp Ile Trp Tyr Leu Ala Gly
 380 385 390
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 Thr Gly Ile

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 <211> 1170
 <212> DNA
 <213> Homo sapiens

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<210> 271
<211> 238
<212> PRT
<213> Homo sapiens

<400> 271
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35 40 45
Val Pro Cys Asp Tyr Asp His Cys Arg His Leu Gln Val Pro Cys
50 55 60
Lys Glu Leu Gln Arg Val Gly Pro Ala Ala Cys Leu Cys Pro Gly
65 70 75

Leu	Ser	Ser	Pro	Ala	Gln	Pro	Pro	Asp	Pro	Pro	Arg	Met	Gly	Glu
80									85					90
Val	Arg	Ile	Ala	Ala	Glu	Glu	Gly	Arg	Ala	Val	Val	His	Trp	Cys
95									100					105
Ala	Pro	Phe	Ser	Pro	Val	Leu	His	Tyr	Trp	Leu	Leu	Leu	Trp	Asp
110									115					120
Gly	Ser	Glu	Ala	Ala	Gln	Lys	Gly	Pro	Pro	Leu	Asn	Ala	Thr	Val
125									130					135
Arg	Arg	Ala	Glu	Leu	Lys	Gly	Leu	Lys	Pro	Gly	Gly	Ile	Tyr	Val
140									145					150
Val	Cys	Val	Val	Ala	Ala	Asn	Glu	Ala	Gly	Ala	Ser	Arg	Val	Pro
155									160					165
Gln	Ala	Gly	Gly	Glu	Gly	Leu	Glu	Gly	Ala	Asp	Ile	Pro	Ala	Phe
170									175					180
Gly	Pro	Cys	Ser	Arg	Leu	Ala	Val	Pro	Pro	Asn	Pro	Arg	Thr	Leu
185									190					195
Val	His	Ala	Ala	Val	Gly	Val	Gly	Thr	Ala	Leu	Ala	Leu	Leu	Ser
200									205					210
Cys	Ala	Ala	Leu	Val	Trp	His	Phe	Cys	Leu	Arg	Asp	Arg	Trp	Gly
215									220					225
Cys	Pro	Arg	Arg	Ala	Ala	Ala	Arg	Ala	Ala	Gly	Ala	Leu		
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<210> 272

<211> 2397

<212> DNA

<213> Homo sapiens

<400> 272

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<210> 273

<211> 305

<212> PRT

<213> Homo sapiens

<400> 273

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					20				25					30

Val	Ser	Ala	Trp	Met	Arg	Asp	Tyr	Leu	Asn	Asn	Val	Leu	Thr	Leu
					35				40					45

Thr	Ala	Glu	Thr	Arg	Val	Glu	Glu	Ala	Val	Ile	Leu	Thr	Tyr	Phe
					50				55					60

Pro	Val	Val	His	Pro	Val	Met	Ile	Ala	Val	Cys	Cys	Phe	Leu	Ile
					65				70					75

Ile	Val	Gly	Met	Leu	Gly	Tyr	Cys	Gly	Thr	Val	Lys	Arg	Asn	Leu
					80				85					90

Leu	Leu	Leu	Ala	Trp	Tyr	Phe	Gly	Ser	Leu	Leu	Val	Ile	Phe	Cys
					95				100					105

Val	Glu	Leu	Ala	Cys	Gly	Val	Trp	Thr	Tyr	Glu	Gln	Glu	Leu	Met
					110				115					120

Val	Pro	Val	Gln	Trp	Ser	Asp	Met	Val	Thr	Leu	Lys	Ala	Arg	Met
					125				130					135

Thr	Asn	Tyr	Gly	Leu	Pro	Arg	Tyr	Arg	Trp	Leu	Thr	His	Ala	Trp
					140				145					150

Asn	Phe	Phe	Gln	Arg	Glu	Phe	Lys	Cys	Cys	Gly	Val	Val	Tyr	Phe
					155				160					165

Thr Asp Trp Leu Glu Met Thr Glu Met Asp Trp Pro Pro Asp Ser

170	175	180
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185	190	195
Glu Asp Leu Ser Asp Leu Tyr Gln Glu Gly Cys Gly Lys Lys Met		
200	205	210
Tyr Ser Phe Leu Arg Gly Thr Lys Gln Leu Gln Val Leu Arg Phe		
215	220	225
Leu Gly Ile Ser Ile Gly Val Thr Gln Ile Leu Ala Met Ile Leu		
230	235	240
Thr Ile Thr Leu Leu Trp Ala Leu Tyr Tyr Asp Arg Arg Glu Pro		
245	250	255
Gly Thr Asp Gln Met Met Ser Leu Lys Asn Asp Asn Ser Gln His		
260	265	270
Leu Ser Cys Pro Ser Val Glu Leu Leu Lys Pro Ser Leu Ser Arg		
275	280	285
Ile Phe Glu His Thr Ser Met Ala Asn Ser Phe Asn Thr His Phe		
290	295	300
Glu Met Glu Glu Leu		
305		

<210> 274
<211> 2063
<212> DNA
<213> Homo sapiens

<400> 274
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<210> 275

<211> 432

<212> PRT

<213> Homo sapiens

<400> 275

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Lys Val Gly Ile Pro Ile Ile Ala Leu Leu Ser Leu Ala Ser
35 40 45

Ile Ile Ile Val Val Val Leu Ile Lys Val Ile Leu Asp Lys Tyr
50 55 60

Tyr Phe Leu Cys Gly Gln Pro Leu His Phe Ile Pro Arg Lys Gln
65 70 75

Leu Cys Asp Gly Glu Leu Asp Cys Pro Leu Gly Glu Asp Glu Glu
80 85 90

His Cys Val Lys Ser Phe Pro Glu Gly Pro Ala Val Ala Val Arg
95 100 105

Leu Ser Lys Asp Arg Ser Thr Leu Gln Val Leu Asp Ser Ala Thr
110 115 120

Gly Asn Trp Phe Ser Ala Cys Phe Asp Asn Phe Thr Glu Ala Leu
125 130 135

Ala Glu Thr Ala Cys Arg Gln Met Gly Tyr Ser Arg Ala Val Glu
140 145 150

Ile Gly Pro Asp Gln Asp Leu Asp Val Val Glu Ile Thr Glu Asn
155 160 165

Ser Gln Glu Leu Arg Met Arg Asn Ser Ser Gly Pro Cys Leu Ser
170 175 180

Gly Ser Leu Val Ser Leu His Cys Leu Ala Cys Gly Lys Ser Leu
185 190 195

Lys Thr Pro Arg Val Val Gly Gly Glu Ala Ser Val Asp Ser
200 205 210

Trp Pro Trp Gln Val Ser Ile Gln Tyr Asp Lys Gln His Val Cys
215 220 225

Gly Gly Ser Ile Leu Asp Pro His Trp Val Leu Thr Ala Ala His
230 235 240

Cys Phe Arg Lys His Thr Asp Val Phe Asn Trp Lys Val Arg Ala
245 250 255

Gly Ser Asp Lys Leu Gly Ser Phe Pro Ser Leu Ala Val Ala Lys
 260 265 270
 Ile Ile Ile Ile Glu Phe Asn Pro Met Tyr Pro Lys Asp Asn Asp
 275 280 285
 Ile Ala Leu Met Lys Leu Gln Phe Pro Leu Thr Phe Ser Gly Thr
 290 295 300
 Val Arg Pro Ile Cys Leu Pro Phe Phe Asp Glu Glu Leu Thr Pro
 305 310 315
 Ala Thr Pro Leu Trp Ile Ile Gly Trp Gly Phe Thr Lys Gln Asn
 320 325 330
 Gly Gly Lys Met Ser Asp Ile Leu Leu Gln Ala Ser Val Gln Val
 335 340 345
 Ile Asp Ser Thr Arg Cys Asn Ala Asp Asp Ala Tyr Gln Gly Glu
 350 355 360
 Val Thr Glu Lys Met Met Cys Ala Gly Ile Pro Glu Gly Gly Val
 365 370 375
 Asp Thr Cys Gln Gly Asp Ser Gly Gly Pro Leu Met Tyr Gln Ser
 380 385 390
 Asp Gln Trp His Val Val Gly Ile Val Ser Trp Gly Tyr Gly Cys
 395 400 405
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 410 415 420
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 <212> DNA
 <213> Homo sapiens
 <400> 276
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<210> 277

<211> 761

<212> PRT

<213> Homo sapiens

<400> 277

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 20 25 30

Ala Gly Gly Gly Gln Gly Pro Met Pro Arg Val Arg Tyr Tyr
 35 40 45

Ala Gly Asp Glu Arg Arg Ala Leu Ser Phe Phe His Gln Lys Gly
 50 55 60

Leu Gln Asp Phe Asp Thr Leu Leu Ser Gly Asp Gly Asn Thr
 65 70 75

Leu Tyr Val Gly Ala Arg Glu Ala Ile Leu Ala Leu Asp Ile Gln
 80 85 90

Asp Pro Gly Val Pro Arg Leu Lys Asn Met Ile Pro Trp Pro Ala
 95 100 105

Ser Asp Arg Lys Lys Ser Glu Cys Ala Phe Lys Lys Lys Ser Asn
 110 115 120

Glu Thr Gln Cys Phe Asn Phe Ile Arg Val Leu Val Ser Tyr Asn
 125 130 135

Val Thr His Leu Tyr Thr Cys Gly Thr Phe Ala Phe Ser Pro Ala
 140 145 150

Cys Thr Phe Ile Glu Leu Gln Asp Ser Tyr Leu Leu Pro Ile Ser
 155 160 165

Glu Asp Lys Val Met Glu Gly Lys Gly Gln Ser Pro Phe Asp Pro
 170 175 180

Ala His Lys His Thr Ala Val Leu Val Asp Gly Met Leu Tyr Ser
 185 190 195

Gly Thr Met Asn Asn Phe Leu Gly Ser Glu Pro Ile Leu Met Arg
 200 205 210

Thr Leu Gly Ser Gln Pro Val Leu Lys Thr Asp Asn Phe Leu Arg
 215 220 225

Trp Leu His His Asp Ala Ser Phe Val Ala Ala Ile Pro Ser Thr
 230 235 240

Gln Val Val Tyr Phe Phe Phe Glu Glu Thr Ala Ser Glu Phe Asp
 245 250 255

Phe Phe Glu Arg Leu His Thr Ser Arg Val Ala Arg Val Cys Lys
 260 265 270

Asn Asp Val Gly Gly Glu Lys Leu Leu Gln Lys Lys Trp Thr Thr
 275 280 285

Phe Leu Lys Ala Gln Leu Leu Cys Thr Gln Pro Gly Gln Leu Pro

290	295	300
Phe Asn Val Ile Arg His Ala Val Leu	Leu Pro Ala Asp Ser	Pro
305	310	315
Thr Ala Pro His Ile Tyr Ala Val Phe	Thr Ser Gln Trp Gln Val	
320	325	330
Gly Gly Thr Arg Ser Ser Ala Val Cys	Ala Phe Ser Leu Leu Asp	
335	340	345
Ile Glu Arg Val Phe Lys Gly Lys Tyr	Lys Glu Leu Asn Lys Glu	
350	355	360
Thr Ser Arg Trp Thr Thr Tyr Arg Gly	Pro Glu Thr Asn Pro Arg	
365	370	375
Pro Gly Ser Cys Ser Val Gly Pro Ser	Ser Asp Lys Ala Leu Thr	
380	385	390
Phe Met Lys Asp His Phe Leu Met Asp	Glu Gln Val Val Gly Thr	
395	400	405
Pro Leu Leu Val Lys Ser Gly Val Glu	Tyr Thr Arg Leu Ala Val	
410	415	420
Glu Thr Ala Gln Gly Leu Asp Gly His	Ser His Leu Val Met Tyr	
425	430	435
Leu Gly Thr Thr Gly Ser Leu His Lys	Ala Val Val Ser Gly	
440	445	450
Asp Ser Ser Ala His Leu Val Glu Glu	Ile Gln Leu Phe Pro Asp	
455	460	465
Pro Glu Pro Val Arg Asn Leu Gln Leu	Ala Pro Thr Gln Gly Ala	
470	475	480
Val Phe Val Gly Phe Ser Gly Gly Val	Trp Arg Val Pro Arg Ala	
485	490	495
Asn Cys Ser Val Tyr Glu Ser Cys Val	Asp Cys Val Leu Ala Arg	
500	505	510
Asp Pro His Cys Ala Trp Asp Pro Glu	Ser Arg Thr Cys Cys Leu	
515	520	525
Leu Ser Ala Pro Asn Leu Asn Ser Trp	Lys Gln Asp Met Glu Arg	
530	535	540
Gly Asn Pro Glu Trp Ala Cys Ala Ser	Gly Pro Met Ser Arg Ser	
545	550	555
Leu Arg Pro Gln Ser Arg Pro Gln Ile	Ile Lys Glu Val Leu Ala	
560	565	570
Val Pro Asn Ser Ile Leu Glu Leu Pro	Cys Pro His Leu Ser Ala	
575	580	585

Leu Ala Ser Tyr Tyr Trp Ser His Gly Pro Ala Ala Val Pro Glu
590 595 600

Ala Ser Ser Thr Val Tyr Asn Gly Ser Leu Leu Leu Ile Val Gln
605 610 615

Asp Gly Val Gly Gly Leu Tyr Gln Cys Trp Ala Thr Glu Asn Gly
620 625 630

Phe Ser Tyr Pro Val Ile Ser Tyr Trp Val Asp Ser Gln Asp Gln
635 640 645

Thr Leu Ala Leu Asp Pro Glu Leu Ala Gly Ile Pro Arg Glu His
650 655 660

Val Lys Val Pro Leu Thr Arg Val Ser Gly Gly Ala Ala Leu Ala
665 670 675

Ala Gln Gln Ser Tyr Trp Pro His Phe Val Thr Val Thr Val Leu
680 685 690

Phe Ala Leu Val Leu Ser Gly Ala Leu Ile Ile Leu Val Ala Ser
695 700 705

Pro Leu Arg Ala Leu Arg Ala Arg Gly Lys Val Gln Gly Cys Glu
710 715 720

Thr Leu Arg Pro Gly Glu Lys Ala Pro Leu Ser Arg Glu Gln His
725 730 735

Leu Gln Ser Pro Lys Glu Cys Arg Thr Ser Ala Ser Asp Val Asp
740 745 750

Ala Asp Asn Asn Cys Leu Gly Thr Glu Val Ala
755 760

<210> 278

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 278

ctgctggta aatctggcgt ggag 24

<210> 279

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 279
gtctggcct ggctgtccac ccag 24

<210> 280
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 280
catttgtca tgtacctggg aaccaccaca gggtcgctcc acaag 45

<210> 281
<211> 2320
<212> DNA
<213> Homo sapiens

<400> 281
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atctacagta ggtgaaagcc attatctact gatggaccgg gtttctcaga 200
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ccttttatgc cagattttaa aaaggaagaa aaatcatatc aagtttatcg 300
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<210> 282
<211> 523
<212> PRT
<213> Homo sapiens

<400> 282
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20 25 30
Val Gly Gly Ser His Tyr Leu Leu Met Asp Arg Val Ser Gln Ile
35 40 45
Leu Gln Asp His Gly His Asn Val Thr Met Leu Asn His Lys Arg
50 55 60
Gly Pro Phe Met Pro Asp Phe Lys Lys Glu Glu Lys Ser Tyr Gln
65 70 75
Val Ile Ser Trp Leu Ala Pro Glu Asp His Gln Arg Glu Phe Lys
80 85 90
Lys Ser Phe Asp Phe Phe Leu Glu Glu Thr Leu Gly Gly Arg Gly
95 100 105
Lys Phe Glu Asn Leu Leu Asn Val Leu Glu Tyr Leu Ala Leu Gln
110 115 120
Cys Ser His Phe Leu Asn Arg Lys Asp Ile Met Asp Ser Leu Lys
125 130 135
Asn Glu Asn Phe Asp Met Val Ile Val Glu Thr Phe Asp Tyr Cys
140 145 150
Pro Phe Leu Ile Ala Glu Lys Leu Gly Lys Pro Phe Val Ala Ile
155 160 165
Leu Ser Thr Ser Phe Gly Ser Leu Glu Phe Gly Leu Pro Ile Pro
170 175 180
Leu Ser Tyr Val Pro Val Phe Arg Ser Leu Leu Thr Asp His Met
185 190 195
Asp Phe Trp Gly Arg Val Lys Asn Phe Leu Met Phe Phe Ser Phe
200 205 210
Cys Arg Arg Gln Gln His Met Gln Ser Thr Phe Asp Asn Thr Ile
215 220 225
Lys Glu His Phe Thr Glu Gly Ser Arg Pro Val Leu Ser His Leu
230 235 240
Leu Leu Lys Ala Glu Leu Trp Phe Ile Asn Ser Asp Phe Ala Phe
245 250 255
Asp Phe Ala Arg Pro Leu Leu Pro Asn Thr Val Tyr Val Gly Gly

	260	265	270
Leu Met Glu Lys Pro Ile Lys Pro Val Pro Gln Asp Leu Glu Asn			
275	280	285	
Phe Ile Ala Lys Phe Gly Asp Ser Gly Phe Val Leu Val Thr Leu			
290	295	300	
Gly Ser Met Val Asn Thr Cys Gln Asn Pro Glu Ile Phe Lys Glu			
305	310	315	
Met Asn Asn Ala Phe Ala His Leu Pro Gln Gly Val Ile Trp Lys			
320	325	330	
Cys Gln Cys Ser His Trp Pro Lys Asp Val His Leu Ala Ala Asn			
335	340	345	
Val Lys Ile Val Asp Trp Leu Pro Gln Ser Asp Leu Leu Ala His			
350	355	360	
Pro Ser Ile Arg Leu Phe Val Thr His Gly Gly Gln Asn Ser Ile			
365	370	375	
Met Glu Ala Ile Gln His Gly Val Pro Met Val Gly Ile Pro Leu			
380	385	390	
Phe Gly Asp Gln Pro Glu Asn Met Val Arg Val Glu Ala Lys Lys			
395	400	405	
Phe Gly Val Ser Ile Gln Leu Lys Lys Leu Lys Ala Glu Thr Leu			
410	415	420	
Ala Leu Lys Met Lys Gln Ile Met Glu Asp Lys Arg Tyr Lys Ser			
425	430	435	
Ala Ala Val Ala Ala Ser Val Ile Leu Arg Ser His Pro Leu Ser			
440	445	450	
Pro Thr Gln Arg Leu Val Gly Trp Ile Asp His Val Leu Gln Thr			
455	460	465	
Gly Gly Ala Thr His Leu Lys Pro Tyr Val Phe Gln Gln Pro Trp			
470	475	480	
His Glu Gln Tyr Leu Phe Asp Val Phe Val Phe Leu Leu Gly Leu			
485	490	495	
Thr Leu Gly Thr Leu Trp Leu Cys Gly Lys Leu Leu Gly Met Ala			
500	505	510	
Val Trp Trp Leu Arg Gly Ala Arg Lys Val Lys Glu Thr			
515	520		

<210> 283
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 283
tgccttgct cacctacccc aagg 24

<210> 284
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 284
tcaggcttgt ctccaaagag aggg 24

<210> 285
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 285
cccaaagatg tccacctggc tgcaaatgtg aaaattgtgg actgg 45

<210> 286
<211> 2340
<212> DNA
<213> Homo sapiens

<400> 286
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cccgtcacac acacatacca tttctccat cccccaggt ccagccctca 150
gtgctgtccc atccagcagg gctaccctga agctctggct gcagccctcc 200
cgtccagtgg gcaggcggct tcatccctcc tttctctccc aaagcccaac 250
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gagtgcctgg tggTCTGTGA gcctggccGA gctgctgcAG gggggCCCGG 650
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tccgaAGCCA ccACCATGAG ccAGCAGGGG aaACCGGCA a tggcaccAGT 750
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tttcaAGCAC aagaatCCAG cccCTGACAA ctTTCTTCTG ccCTCTCTTG 1150
ccccAGAAAC agcAGAGGCA ggAGAGAGAC tccCTCTGGC tcCTATCCCA 1200
cctctttGCA tgggaccCTG tgccAAACAC ccaAGTTAA gagaAGAGTA 1250
gagCTGTGGC atctccAGAC caggCCTTC caccCACCCa ccccccAGTTA 1300
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ctccggTTCC cccACCCCCAG ctTCCtGCTC aatgctGATC agggacAGGT 1450
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tgagtGTGTT tgctctGGCT gagAGCAGAG ctgagAGCAG gtatacAGAG 1850
ctggaAGTGG accatGGAAA acatcgataa ccatgcatcc tcttgcttgg 1900

ccacacctcg aaactgctcc acctttgaag tttgaacttt agtccctcca 1950
cactctgact gctgcctcct tcctcccagc tctctcaactg agttatcttc 2000
actgtacctg ttccagcata tccccactat ctctcttct cctgatctgt 2050
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tcttatccccg ctgtcccatt ggcccagcct ggatgaatct atcaataaaa 2200
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<210> 287

<211> 205

<212> PRT

<213> Homo sapiens

<400> 287

Met	Leu	Gly	Ala	Lys	Pro	His	Trp	Leu	Pro	Gly	Pro	Leu	His	Ser
1				5				10					15	

Pro	Gly	Leu	Pro	Leu	Val	Leu	Val	Leu	Leu	Ala	Leu	Gly	Ala	Gly
		20						25				30		

Trp	Ala	Gln	Glu	Gly	Ser	Glu	Pro	Val	Leu	Leu	Glu	Gly	Glu	Cys
		35						40				45		

Leu	Val	Val	Cys	Glu	Pro	Gly	Arg	Ala	Ala	Gly	Gly	Pro	Gly	
			50					55				60		

Gly	Ala	Ala	Leu	Gly	Glu	Ala	Pro	Pro	Gly	Arg	Val	Ala	Phe	Ala
			65					70				75		

Ala	Val	Arg	Ser	His	His	His	Glu	Pro	Ala	Gly	Glu	Thr	Gly	Asn
				80				85				90		

Gly	Thr	Ser	Gly	Ala	Ile	Tyr	Phe	Asp	Gln	Val	Leu	Val	Asn	Glu
					95				100				105	

Gly	Gly	Gly	Phe	Asp	Arg	Ala	Ser	Gly	Ser	Phe	Val	Ala	Pro	Val
				110				115				120		

Arg	Gly	Val	Tyr	Ser	Phe	Arg	Phe	His	Val	Val	Lys	Val	Tyr	Asn
				125				130				135		

Arg	Gln	Thr	Val	Gln	Val	Ser	Leu	Met	Leu	Asn	Thr	Trp	Pro	Val
					140			145				150		

Ile	Ser	Ala	Phe	Ala	Asn	Asp	Pro	Asp	Val	Thr	Arg	Glu	Ala	Ala
					155				160			165		

Thr Ser Ser Val Leu Leu Pro Leu Asp Pro Gly Asp Arg Val Ser

170

175

180

Leu Arg Leu Arg Arg Gly Asn Leu Leu Gly Gly Trp Lys Tyr Ser
185 190 195

Ser Phe Ser Gly Phe Leu Ile Phe Pro Leu
200 205

<210> 288

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 288

aggcagccac cagctctgtg ctac 24

<210> 289

<211> 27

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-27

<223> Synthetic construct.

<400> 289

cagagaggga agatgaggaa gccagag 27

<210> 290

<211> 42

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-42

<223> Synthetic construct.

<400> 290

ctgtgtact gcccttggac cctggggacc gagtgtctct gc 42

<210> 291

<211> 1570

<212> DNA

<213> Homo sapiens

<400> 291

gctgttttctc tcgcgccacc actggccgcc ggccgcagct ccaggtgtcc 50

tagccgccca gcctcgacgc cgtcccggga cccctgtgct ctgcgcgaag 100

ccctggcccc gggggccggg gcatggccca ggggcgcggg gtgaagcggc 150

ttcccgcggg gccgtgactg ggcgggcttc agccatgaag accctcatag 200
ccgcctactc cggggtcctg cgcggcgagc gtcaggccga ggctgaccgg 250
agccagcgct ctacacggagg acctgcgctg tcgcgcgagg ggtctggag 300
atggggcact ggatccagca tcctctccgc cctccaggac ctcttctctg 350
tcacacctggct caatagggtcc aagggtggaaa agcagactaca ggtcatctca 400
gtgctccagt gggctctgtc cttccttgta ctggagtggt cctgcagtgc 450
catcctcatg tacatattct gcactgattt ctggctcatc gctgtgctct 500
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agagcccatc accatccccca agctggagca cccaaacccag caagacatcg 1250
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cacaagacca agttcggcct cccggagact gaggtcctgg aggtgaactg 1350
agccagcctt cggggccaat tccctggagg aaccagctgc aaatcacttt 1400
tttgctctgt aaatttgaa gtgtcatgg tgcgtgtgg ttatTTaaaa 1450
gaaattataa caattttgct aaaccaaaaa aaaaaaaaaa aaaaaaaaaa 1500
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1550
aaaaaaaaaa aaaaaaaaaa 1570

<210> 292
 <211> 388
 <212> PRT
 <213> Homo sapiens

<400> 292
 Met Lys Thr Leu Ile Ala Ala Tyr Ser Gly Val Leu Arg Gly Glu
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Arg Gln Ala Glu Ala Asp Arg Ser Gln Arg Ser His Gly Gly Pro
 20 25 30

Ala Leu Ser Arg Glu Gly Ser Gly Arg Trp Gly Thr Gly Ser Ser
 35 40 45

Ile Leu Ser Ala Leu Gln Asp Leu Phe Ser Val Thr Trp Leu Asn
 50 55 60

Arg Ser Lys Val Glu Lys Gln Leu Gln Val Ile Ser Val Leu Gln
 65 70 75

Trp Val Leu Ser Phe Leu Val Leu Gly Val Ala Cys Ser Ala Ile
 80 85 90

Leu Met Tyr Ile Phe Cys Thr Asp Cys Trp Leu Ile Ala Val Leu
 95 100 105

Tyr Phe Thr Trp Leu Val Phe Asp Trp Asn Thr Pro Lys Lys Gly
 110 115 120

Gly Arg Arg Ser Gln Trp Val Arg Asn Trp Ala Val Trp Arg Tyr
 125 130 135

Phe Arg Asp Tyr Phe Pro Ile Gln Leu Val Lys Thr His Asn Leu
 140 145 150

Leu Thr Thr Arg Asn Tyr Ile Phe Gly Tyr His Pro His Gly Ile
 155 160 165

Met Gly Leu Gly Ala Phe Cys Asn Phe Ser Thr Glu Ala Thr Glu
 170 175 180

Val Ser Lys Lys Phe Pro Gly Ile Arg Pro Tyr Leu Ala Thr Leu
 185 190 195

Ala Gly Asn Phe Arg Met Pro Val Leu Arg Glu Tyr Leu Met Ser
 200 205 210

Gly Gly Ile Cys Pro Val Ser Arg Asp Thr Ile Asp Tyr Leu Leu
 215 220 225

Ser Lys Asn Gly Ser Gly Asn Ala Ile Ile Ile Val Val Gly Gly
 230 235 240

Ala Ala Glu Ser Leu Ser Ser Met Pro Gly Lys Asn Ala Val Thr
 245 250 255

Leu Arg Asn Arg Lys Gly Phe Val Lys Leu Ala Leu Arg His Gly

260	265	270
Ala Asp Leu Val Pro Ile Tyr Ser Phe Gly Glu Asn Glu Val Tyr		
275	280	285
Lys Gln Val Ile Phe Glu Glu Gly Ser Trp Gly Arg Trp Val Gln		
290	295	300
Lys Lys Phe Gln Lys Tyr Ile Gly Phe Ala Pro Cys Ile Phe His		
305	310	315
Gly Arg Gly Leu Phe Ser Ser Asp Thr Trp Gly Leu Val Pro Tyr		
320	325	330
Ser Lys Pro Ile Thr Thr Val Val Gly Glu Pro Ile Thr Ile Pro		
335	340	345
Lys Leu Glu His Pro Thr Gln Gln Asp Ile Asp Leu Tyr His Thr		
350	355	360
Met Tyr Met Glu Ala Leu Val Lys Leu Phe Asp Lys His Lys Thr		
365	370	375
Lys Phe Gly Leu Pro Glu Thr Glu Val Leu Glu Val Asn		
380	385	

<210> 293
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 293
gctgacacctgg ttcccatcta ctcc 24

<210> 294
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 294
cccacagaca cccatgacac ttcc 24

<210> 295
<211> 50
<212> DNA
<213> Artificial

<220>

<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 295
aagaatgaat tgtacaaagc aggtgatctt cgaggaggc tcctggggcc 50

<210> 296
<211> 3060
<212> DNA
<213> Homo sapiens

<400> 296
gggcggcggg atggggcccg gggcggcgg ggcggcact cgctgaggcc 50
ccgacgcagg gccgggcccgg gcccagggcc gaggagcgcg gcggccagag 100
cggggccgcg gagggcgcgc cggggacgcc cgcgcacga gcaggtggcg 150
gcggctgcag gcttgtccag ccggaaagccc tgagggcagc tggccact 200
ggctctgctg accttgtgcc ttggacggct gtcctcagcg aggggcccgtg 250
cacccgcctcc tgagcagcgc catgggcctg ctggccttcc tgaagaccca 300
gttcgtgctg cacctgctgg tcggcttgc cttcgtggc agtggcttg 350
tcatcaactt cgtccagctg tgcacgcctgg cgctctggcc ggtcagcaag 400
cagctctacc gccgcctcaa ctgcccctc gcctactcac tctggagcca 450
actggtcatg ctgctggagt ggtggcctcg cacggagtgt acactgttca 500
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ctcaaccaca acttcgagat cgacttcctc tgggggtggga ccatgtgtga 600
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tctacgtgcc cctcatcgcc tggacgtggc actttctggaa gattgtgttc 700
tgcaagcggaa agtgggagga ggaccggac accgtggc'cg aaggagctgag 750
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gctaaggggc ttccctgtcct caagtaccac ctgctgccgc ggaccaaggg 900
cttcaccacc gcagtcaagt gcctccgggg gacagtcgcgac gctgtctatg 950
atgtaaccct gaacttcaga ggaaacaaga acccgccct gctggggatc 1000
ctctacggaa agaagtacga ggcggacatg tgcgtgagga gatttcctct 1050
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tgtaccagga gaaggacgcg ctccaggaga tatataatca gaagggcatg 1150

tttccagggg agcagttaa gcctgcccgg aggccgtgga ccctcctgaa 1200
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catatgcattt atgagagtcc cagaaggaga ggagagaaaag ggtcagaaaag 1700
aatggccaca agctgatgaa aaacagtaac ctacccactc aggaagctca 1750
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aatcaaagtg tcaaattgaca aagaatctt aaagcagcaa gagatgagca 1850
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cagaaatcat gggagccagg agatagtggg atgaacactg ttgaaggcaa 1950
aaccttcaac tgtaattatt ggactttga gtcttagatg gtcctgac 2000
ctttgtcttc agggacagtt ttcaattta atccctaata acaattagtc 2050
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agctcaagtg atctgcctgc ttcagcctcc caaagtgc tgattacaga 2850
catgagccac tgcacctggc aaactccaa aattcaacac acacacacaa 2900
aaaaccacct gattcaaat gggcagaggg gcccgggtgtg gcccccaacta 2950
ccagggagac tgaagtggga ggatcgctt ggcattgagaa gtcgaggctg 3000
cagtgagtcg aggttgtgcg actgcattcc agcctggaca acagagttag 3050
accctgtctc 3060

<210> 297

<211> 368

<212> PRT

<213> Homo sapiens

<400> 297

Met Gly Leu Leu Ala Phe Leu Lys Thr Gln Phe Val Leu His Leu
1 5 10 15

Leu Val Gly Phe Val Phe Val Val Ser Gly Leu Val Ile Asn Phe
20 25 30

Val Gln Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln Leu
35 40 45

Tyr Arg Arg Leu Asn Cys Arg Leu Ala Tyr Ser Leu Trp Ser Gln
50 55 60

Leu Val Met Leu Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu
65 70 75

Phe Thr Asp Gln Ala Thr Val Glu Arg Phe Gly Lys Glu His Ala
80 85 90

Val Ile Ile Leu Asn His Asn Phe Glu Ile Asp Phe Leu Cys Gly
95 100 105

Trp Thr Met Cys Glu Arg Phe Gly Val Leu Gly Ser Ser Lys Val
110 115 120

Leu Ala Lys Lys Glu Leu Leu Tyr Val Pro Leu Ile Gly Trp Thr
125 130 135

Trp Tyr Phe Leu Glu Ile Val Phe Cys Lys Arg Lys Trp Glu Glu
140 145 150

Asp Arg Asp Thr Val Val Glu Gly Leu Arg Arg Leu Ser Asp Tyr
155 160 165

Pro	Glu	Tyr	Met	Trp	Phe	Leu	Leu	Tyr	Cys	Glu	Gly	Thr	Arg	Phe
				170					175				180	
Thr	Glu	Thr	Lys	His	Arg	Val	Ser	Met	Glu	Val	Ala	Ala	Ala	Lys
				185					190				195	
Gly	Leu	Pro	Val	Leu	Lys	Tyr	His	Leu	Leu	Pro	Arg	Thr	Lys	Gly
				200					205				210	
Phe	Thr	Thr	Ala	Val	Lys	Cys	Leu	Arg	Gly	Thr	Val	Ala	Ala	Val
				215					220				225	
Tyr	Asp	Val	Thr	Leu	Asn	Phe	Arg	Gly	Asn	Lys	Asn	Pro	Ser	Leu
				230					235				240	
Leu	Gly	Ile	Leu	Tyr	Gly	Lys	Lys	Tyr	Glu	Ala	Asp	Met	Cys	Val
				245					250				255	
Arg	Arg	Phe	Pro	Leu	Glu	Asp	Ile	Pro	Leu	Asp	Glu	Lys	Glu	Ala
				260					265				270	
Ala	Gln	Trp	Leu	His	Lys	Leu	Tyr	Gln	Glu	Lys	Asp	Ala	Leu	Gln
				275					280				285	
Glu	Ile	Tyr	Asn	Gln	Lys	Gly	Met	Phe	Pro	Gly	Glu	Gln	Phe	Lys
				290					295				300	
Pro	Ala	Arg	Arg	Pro	Trp	Thr	Leu	Leu	Asn	Phe	Leu	Ser	Trp	Ala
				305					310				315	
Thr	Ile	Leu	Leu	Ser	Pro	Leu	Phe	Ser	Phe	Val	Leu	Gly	Val	Phe
				320					325				330	
Ala	Ser	Gly	Ser	Pro	Leu	Leu	Ile	Leu	Thr	Phe	Leu	Gly	Phe	Val
				335					340				345	
Gly	Ala	Ala	Ser	Phe	Gly	Val	Arg	Arg	Ile	Ile	Gly	Glu	Ser	Leu
				350					355				360	
Glu	Pro	Gly	Arg	Trp	Arg	Leu	Gln							
				365										

<210> 298

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 298

cttcctctgt gggtgacca tgtg 24

<210> 299

<211> 21

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-21

<223> Synthetic construct.

<400> 299
gccaccca tgctaacgcg g 21

<210> 300

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 300
ccaaggcct cgctaagaag gagctgctct acgtccccct catcg 45

<210> 301

<211> 1334

<212> DNA

<213> Homo sapiens

<400> 301
gatattcttt attttaaga atctgaagta ctatgcatca ctccctccaa 50
tgtcctgggg cagccaccag gcatattcat ctttggtgt gtttttcttt 100
tgcttttagca ctggggcact tcttgcttat ttctttggta ggaaagggc 150
tcagtttgc ttgtggggtt ggtggcaggc aggccggctt acgcctgata 200
cggccctggg ttagaaggga agggaagata aactttata caaatgggaa 250
tagctggggt ctgagacctg cttcctcagt aaaattcctg ggatctgcct 300
ataccttctt ttctctaacc tggcataccc tgcttaaägc ctctcaggc 350
ttctctctgt tcttaggatc aaagtattta gagctacaag agccctcatg 400
gtctggcccc tgccccctg gccagctca ttgtacatgt ggtgttctct 450
tgtcggtcct gtaatgtggt atgccatggg gtcttgac aagccttcc 500
tctttggctg gacactgttc cctgcccccc ccatactctt cctacttaat 550
atgttagtcat cctgcagatt tcaattctaa catcatttc tccagggatc 600
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ttcccttttg cagcacttgc cactcagttg tatctttatg tgcgtttgtg 700
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agggtcaagg gcattgctgt gcctgccagg tatagtgcct acatgtggtg 800
ggtgctcatg ttttagagac taaatggagg aggagatgag gaaaagattg 850
aaatctctca gttcaccaga tggtgttaggg cccagcattg taaattcaca 900
cgttgactgt gcttgtaat tatctggga tgcaaggctt gattcagtag 950
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gtccccagcta cttgggaggc tgaagcaaga gaatcgctt aacctgggag 1250
gcggaggttg cagtgagccg agatcaggcc actgtattcc aaccagggtg 1300
acagagttag actctatgtc caaaaaaaaaaaaa 1334

<210> 302

<211> 143

<212> PRT

<213> Homo sapiens

<400> 302

Met His His Ser Leu Gln Cys Pro Gly Ala Ala Thr Arg His Ile
1 5 10 15

His Leu Cys Val Cys Phe Ser Phe Ala Leu Ala Leu Gly His Phe
20 25 30

Leu Leu Ile Ser Leu Val Gly Lys Gly Leu Ser Leu Ser Cys Gly
35 40 45

Val Gly Gly Arg Gln Ala Gly Leu Arg Leu Ile Arg Pro Trp Val
50 55 60

Arg Arg Glu Gly Lys Ile Asn Phe Tyr Thr Asn Gly Asp Ser Trp
65 70 75

Gly Leu Arg Pro Ala Ser Ser Val Lys Phe Leu Gly Ser Ala Tyr
80 85 90

Thr Phe Phe Ser Leu Thr Trp His Thr Leu Leu Lys Ala Ser Gln
95 100 105

Gly Phe Ser Leu Phe Leu Gly Ser Lys Tyr Leu Glu Leu Gln Glu
110 115 120

Pro Ser Trp Ser Gly Pro Cys Pro Pro Gly Gln Leu His Cys Thr
125 130 135

Cys Gly Val Leu Leu Ser Phe Leu

<210> 303
 <211> 1768
 <212> DNA
 <213> Homo sapiens

<400> 303
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 aagggtgtgt gattatagggt gtaagccacc gtgtctggcc tctgaacaac 100
 ttttcagca actaaaaaaag ccacaggagt tgaactgcta ggattctgac 150
 tatgctgtgg tggctagtgc tcctactcct acctacatta aaatctgttt 200
 tttgttctct tgtaactagc ctttaccttc ctaacacaga ggatctgtca 250
 ctgtggctct ggcccaaacc tgaccttcac tctggaacga gaacagaggt 300
 ttctaccac accgtccccct cgaagccggg gacagcctca ctttgctggc 350
 ctctcgctgg agcagtgcac tcaccaactg tctcacgtct ggaggcactg 400
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 ggcatggct cccactgccc aggcattcagc cttgtgttag tcaatcactg 550
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 gctgtggctc agacccagaa ggggtctgt tagaccacctt ggttatgtg 750
 acaggacttgc catttcctg gaacatgagg gaacgcccggaa ggaaagcaaa 800
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 ggaaggctg ccgatggcgc atgacacactt cgggactcac ctctggggcc 950
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 agcaagacat agctgacagg ggctaatggc tcagtgtgg cccaggaggt 1200
 cagcaaggcc tgagagctga tcagaaggc ctgctgtgcg aacacggaaa 1250

tgcctccagt aagcacaggc tgcaaaatcc ccaggcaaag gactgtgtgg 1300
ctcaatttaa atcatgttct agtaattgga gctgtccccca agaccaaagg 1350
agcttagagct tggttcaaat gatctccaag ggcccttata ccccaggaga 1400
ctttgatttg aatttggaaac cccaaatcca aacctaaagaa ccaggtgcat 1450
taagaatcag ttattgccgg gtgtggtggc ctgtaatgcc aacattttgg 1500
gaggccgagg cggttagatc acctgaggtc aggagttcaa gaccagcctg 1550
gccaacatgg tgaaacccct gtctctacta aaaatacaaa aaaactagcc 1600
aggcatggtg gtgtgtgcct gtatcccagc tactcgggag gctgagacag 1650
gagaattact tgaacctggg aggtgaagga ggctgagaca ggagaatcac 1700
ttcagcctga gcaacacagc gagactctgt ctcagaaaaa ataaaaaaaaag 1750
aattatggtt atttgtaa 1768

<210> 304

<211> 109

<212> PRT

<213> Homo sapiens

<400> 304

Met	Leu	Trp	Trp	Leu	Val	Leu	Leu	Leu	Pro	Thr	Leu	Lys	Ser
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Val	Phe	Cys	Ser	Leu	Val	Thr	Ser	Leu	Tyr	Leu	Pro	Asn	Thr	Glu
				20				25				30		

Asp	Leu	Ser	Leu	Trp	Leu	Trp	Pro	Lys	Pro	Asp	Leu	His	Ser	Gly
				35				40				45		

Thr	Arg	Thr	Glu	Val	Ser	Thr	His	Thr	Val	Pro	Ser	Lys	Pro	Gly
				50				55				60		

Thr	Ala	Ser	Pro	Cys	Trp	Pro	Leu	Ala	Gly	Ala	Val	Pro	Ser	Pro
				65				70	"			75		

Thr	Val	Ser	Arg	Leu	Glu	Ala	Leu	Thr	Arg	Ala	Val	Gln	Val	Ala
				80				85				90		

Glu	Pro	Leu	Gly	Ser	Cys	Gly	Phe	Gln	Gly	Gly	Pro	Cys	Pro	Gly
				95				100				105		

Arg Arg Arg Asp

<210> 305

<211> 989

<212> DNA

<213> Homo sapiens

<400> 305

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 ccgccttcgc cactggcctc ttccctggga ggcgggtgccc cccatggcga 200
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<210> 306

<211> 262

<212> PRT

<213> Homo sapiens

<400> 306

Met	Thr	Gln	Pro	Val	Pro	Arg	Leu	Ser	Val	Pro	Ala	Ala	Leu	Ala
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Leu	Gly	Ser	Ala	Ala	Leu	Gly	Ala	Ala	Phe	Ala	Thr	Gly	Leu	Phe
					20				25				30	
Leu	Gly	Arg	Arg	Cys	Pro	Pro	Trp	Arg	Gly	Arg	Arg	Glu	Gln	Cys
				35				40					45	
Leu	Leu	Pro	Pro	Glu	Asp	Ser	Arg	Leu	Trp	Gln	Tyr	Leu	Leu	Ser
				50				55					60	

Arg Ser Met Arg Glu His Pro Ala Leu Arg Ser Leu Arg Leu Leu
 65 70 75
 Thr Leu Glu Gln Pro Gln Gly Asp Ser Met Met Thr Cys Glu Gln
 80 85 90
 Ala Gln Leu Leu Ala Asn Leu Ala Arg Leu Ile Gln Ala Lys Lys
 95 100 105
 Ala Leu Asp Leu Gly Thr Phe Thr Gly Tyr Ser Ala Leu Ala Leu
 110 115 120
 Ala Leu Ala Leu Pro Ala Asp Gly Arg Val Val Thr Cys Glu Val
 125 130 135
 Asp Ala Gln Pro Pro Glu Leu Gly Arg Pro Leu Trp Arg Gln Ala
 140 145 150
 Glu Ala Glu His Lys Ile Asp Leu Arg Leu Lys Pro Ala Leu Glu
 155 160 165
 Thr Leu Asp Glu Leu Leu Ala Ala Gly Glu Ala Gly Thr Phe Asp
 170 175 180
 Val Ala Val Val Asp Ala Asp Lys Glu Asn Cys Ser Ala Tyr Tyr
 185 190 195
 Glu Arg Cys Leu Gln Leu Leu Arg Pro Gly Gly Ile Leu Ala Val
 200 205 210
 Leu Arg Val Leu Trp Arg Gly Lys Val Leu Gln Pro Pro Lys Gly
 215 220 225
 Asp Val Ala Ala Glu Cys Val Arg Asn Leu Asn Glu Arg Ile Arg
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 Arg Asp Val Arg Val Tyr Ile Ser Leu Leu Pro Leu Gly Asp Gly
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 Leu Thr Leu Ala Phe Lys Ile
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<210> 308

<211> 671

<212> PRT

<213> Homo sapiens

<400> 308

Met	Pro	His	Ala	Phe	Lys	Pro	Gly	Asp	Leu	Val	Phe	Ala	Lys	Met
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Lys	Gly	Tyr	Pro	His	Trp	Pro	Ala	Arg	Ile	Asp	Asp	Ile	Ala	Asp
					20				25				30	

Gly	Ala	Val	Lys	Pro	Pro	Pro	Asn	Lys	Tyr	Pro	Ile	Phe	Phe	Phe
								35		40			45	

Gly	Thr	His	Glu	Thr	Ala	Phe	Leu	Gly	Pro	Lys	Asp	Leu	Phe	Pro
					50				55				60	

Tyr	Asp	Lys	Cys	Lys	Asp	Lys	Tyr	Gly	Lys	Pro	Asn	Lys	Arg	Lys
					65				70				75	

Gly	Phe	Asn	Glu	Gly	Leu	Trp	Glu	Ile	Gln	Asn	Asn	Pro	His	Ala
					80				85				90	

Ser	Tyr	Ser	Ala	Pro	Pro	Pro	Val	Ser	Ser	Ser	Asp	Ser	Glu	Ala
					95				100				105	

Pro	Glu	Ala	Asn	Pro	Ala	Asp	Gly	Ser	Asp	Ala	Asp	Glu	Asp	Asp
					110				115				120	

Glu	Asp	Arg	Gly	Val	Met	Ala	Val	Thr	Ala	Val	Thr	Ala	Thr	Ala
					125				130				135	

Ala Ser Asp Arg Met Glu Ser Asp Ser Asp Lys Ser Ser

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155	160	165
Val Ser Lys Arg Ala Arg Lys Ala Ser Ser Asp Leu Asp Gln Ala		
170	175	180
Ser Val Ser Pro Ser Glu Glu Glu Asn Ser Glu Ser Ser Ser Glu		
185	190	195
Ser Glu Lys Thr Ser Asp Gln Asp Phe Thr Pro Glu Lys Lys Ala		
200	205	210
Ala Val Arg Ala Pro Arg Arg Gly Pro Leu Gly Gly Arg Lys Lys		
215	220	225
Lys Lys Ala Pro Ser Ala Ser Asp Ser Asp Ser Lys Ala Asp Ser		
230	235	240
Asp Gly Ala Lys Pro Glu Pro Val Ala Met Ala Arg Ser Ala Ser		
245	250	255
Ser Ser Ser Ser Ser Ser Ser Asp Ser Asp Val Ser Val		
260	265	270
Lys Lys Pro Pro Arg Gly Arg Lys Pro Ala Glu Lys Pro Leu Pro		
275	280	285
Lys Pro Arg Gly Arg Lys Pro Lys Pro Glu Arg Pro Pro Ser Ser		
290	295	300
Ser Ser Ser Asp Ser Asp Ser Asp Glu Val Asp Arg Ile Ser Glu		
305	310	315
Trp Lys Arg Arg Asp Glu Ala Arg Arg Glu Leu Glu Ala Arg		
320	325	330
Arg Arg Arg Glu Gln Glu Glu Glu Leu Arg Arg Leu Arg Glu Gln		
335	340	345
Glu Lys Glu Glu Lys Glu Arg Arg Glu Arg Ala Asp Arg Gly		
350	355	360
Glu Ala Glu Arg Gly Ser Gly Gly Ser Ser Gly Asp Glu Leu Arg		
365	370	375
Glu Asp Asp Glu Pro Val Lys Lys Arg Gly Arg Lys Gly Arg Gly		
380	385	390
Arg Gly Pro Pro Ser Ser Ser Asp Ser Glu Pro Glu Ala Glu Leu		
395	400	405
Glu Arg Glu Ala Lys Lys Ser Ala Lys Lys Pro Gln Ser Ser Ser		
410	415	420
Thr Glu Pro Ala Arg Lys Pro Gly Gln Lys Glu Lys Arg Val Arg		
425	430	435

Pro Glu Glu Lys Gln Gln Ala Lys Pro Val Lys Val Glu Arg Thr
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 Arg Lys Arg Ser Glu Gly Phe Ser Met Asp Arg Lys Val Glu Lys
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 Lys Lys Glu Pro Ser Val Glu Glu Lys Leu Gln Lys Leu His Ser
 470 475 480
 Glu Ile Lys Phe Ala Leu Lys Val Asp Ser Pro Asp Val Lys Arg
 485 490 495
 Cys Leu Asn Ala Leu Glu Glu Leu Gly Thr Leu Gln Val Thr Ser
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 Gln Ile Leu Gln Lys Asn Thr Asp Val Val Ala Thr Leu Lys Lys
 515 520 525
 Ile Arg Arg Tyr Lys Ala Asn Lys Asp Val Met Glu Lys Ala Ala
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 Glu Val Tyr Thr Arg Leu Lys Ser Arg Val Leu Gly Pro Lys Ile
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 Pro Val Asn Gly Glu Ala Thr Ser Gln Lys Gly Glu Ser Ala Glu
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 Asp Lys Glu His Glu Glu Gly Arg Asp Ser Glu Glu Gly Pro Arg
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 Cys Gly Ser Ser Glu Asp Leu His Asp Ser Val Arg Glu Gly Pro
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<210> 310

<211> 777

<212> PRT

<213> Homo sapiens

<400> 310

Met	Asn	Ala	Asn	Lys	Asp	Glu	Arg	Leu	Lys	Ala	Arg	Ser	Gln	Asp
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Phe	His	Leu	Phe	Pro	Ala	Leu	Met	Met	Leu	Ser	Met	Thr	Met	Leu
							20		25				30	

Phe	Leu	Pro	Val	Thr	Gly	Thr	Leu	Lys	Gln	Asn	Ile	Pro	Arg	Leu
				35				40					45	

Lys	Leu	Thr	Tyr	Lys	Asp	Leu	Leu	Ser	Asn	Ser	Cys	Ile	Pro	
				50				55				60		

Phe	Leu	Gly	Ser	Ser	Glu	Gly	Leu	Asp	Phe	Gln	Thr	Leu	Leu	Leu
				65				70				75		

Asp Glu Glu Arg Gly Arg Leu Leu Leu Gly Ala Lys Asp His Ile

80	85	90												
Phe	Leu	Leu	Ser	Leu	Val	Asp	Leu	Asn	Lys	Asn	Phe	Lys	Lys	Ile
				95				100				105		
Tyr	Trp	Pro	Ala	Ala	Lys	Glu	Arg	Val	Glu	Leu	Cys	Lys	Leu	Ala
				110				115				120		
Gly	Lys	Asp	Ala	Asn	Thr	Glu	Cys	Ala	Asn	Phe	Ile	Arg	Val	Leu
				125				130				135		
Gln	Pro	Tyr	Asn	Lys	Thr	His	Ile	Tyr	Val	Cys	Gly	Thr	Gly	Ala
				140				145				150		
Phe	His	Pro	Ile	Cys	Gly	Tyr	Ile	Asp	Leu	Gly	Val	Tyr	Lys	Glu
				155				160				165		
Asp	Ile	Ile	Phe	Lys	Leu	Asp	Thr	His	Asn	Leu	Glu	Ser	Gly	Arg
				170				175				180		
Leu	Lys	Cys	Pro	Phé	Asp	Pro	Gln	Gln	Pro	Phe	Ala	Ser	Val	Met
				185				190				195		
Thr	Asp	Glu	Tyr	Leu	Tyr	Ser	Gly	Thr	Ala	Ser	Asp	Phe	Leu	Gly
				200				205				210		
Lys	Asp	Thr	Ala	Phe	Thr	Arg	Ser	Leu	Gly	Pro	Thr	His	Asp	His
				215				220				225		
His	Tyr	Ile	Arg	Thr	Asp	Ile	Ser	Glu	His	Tyr	Trp	Leu	Asn	Gly
				230				235				240		
Ala	Lys	Phe	Ile	Gly	Thr	Phe	Ile	Pro	Asp	Thr	Tyr	Asn	Pro	
				245				250				255		
Asp	Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Arg	Glu	Ser	Ser	Gln	Glu	
				260				265				270		
Gly	Ser	Thr	Ser	Asp	Lys	Thr	Ile	Leu	Ser	Arg	Val	Gly	Arg	Val
				275				280				285		
Cys	Lys	Asn	Asp	Val	Gly	Gly	Gln	Arg	Ser	Leu	Ile	Asn	Lys	Trp
				290				295				300		
Thr	Thr	Phe	Leu	Lys	Ala	Arg	Leu	Ile	Cys	Ser	Ile	Pro	Gly	Ser
				305				310				315		
Asp	Gly	Ala	Asp	Thr	Tyr	Phe	Asp	Glu	Leu	Gln	Asp	Ile	Tyr	Leu
				320				325				330		
Leu	Pro	Thr	Arg	Asp	Glu	Arg	Asn	Pro	Val	Val	Tyr	Gly	Val	Phe
				335				340				345		
Thr	Thr	Thr	Ser	Ser	Ile	Phe	Lys	Gly	Ser	Ala	Val	Cys	Val	Tyr
				350				355				360		
Ser	Met	Ala	Asp	Ile	Arg	Ala	Val	Phe	Asn	Gly	Pro	Tyr	Ala	His
				365				370				375		

Lys Glu Ser Ala Asp His Arg Trp Val Gln Tyr Asp Gly Arg Ile
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 Pro Tyr Pro Arg Pro Gly Thr Cys Pro Ser Lys Thr Tyr Asp Pro
 395 400 405
 Leu Ile Lys Ser Thr Arg Asp Phe Pro Asp Asp Val Ile Ser Phe
 410 415 420
 Ile Lys Arg His Ser Val Met Tyr Lys Ser Val Tyr Pro Val Ala
 425 430 435
 Gly Gly Pro Thr Phe Lys Arg Ile Asn Val Asp Tyr Arg Leu Thr
 440 445 450
 Gln Ile Val Val Asp His Val Ile Ala Glu Asp Gly Gln Tyr Asp
 455 460 465
 Val Met Phe Leu Gly Thr Asp Ile Gly Thr Val Leu Lys Val Val
 470 475 480
 Ser Ile Ser Lys Glu Lys Trp Asn Met Glu Glu Val Val Leu Glu
 485 490 495
 Glu Leu Gln Ile Phe Lys His Ser Ser Ile Ile Leu Asn Met Glu
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 Leu Ser Leu Lys Gln Gln Gln Leu Tyr Ile Gly Ser Arg Asp Gly
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 Leu Val Gln Leu Ser Leu His Arg Cys Asp Thr Tyr Gly Lys Ala
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 Cys Ala Asp Cys Cys Leu Ala Arg Asp Pro Tyr Cys Ala Trp Asp
 545 550 555
 Gly Asn Ala Cys Ser Arg Tyr Ala Pro Thr Ser Lys Arg Arg Ala
 560 565 570
 Arg Arg Gln Asp Val Lys Tyr Gly Asp Pro Ile Thr Gln Cys Trp
 575 580 585
 Asp Ile Glu Asp Ser Ile Ser His Glu Thr Ala Asp Glu Lys Val
 590 595 600
 Ile Phe Gly Ile Glu Phe Asn Ser Thr Phe Leu Glu Cys Ile Pro
 605 610 615
 Lys Ser Gln Gln Ala Thr Ile Lys Trp Tyr Ile Gln Arg Ser Gly
 620 625 630
 Asp Glu His Arg Glu Glu Leu Lys Pro Asp Glu Arg Ile Ile Lys
 635 640 645
 Thr Glu Tyr Gly Leu Leu Ile Arg Ser Leu Gln Lys Lys Asp Ser
 650 655 660
 Gly Met Tyr Tyr Cys Lys Ala Gln Glu His Thr Phe Ile His Thr

665	670	675
Ile Val Lys Leu Thr Leu Asn Val Ile Glu Asn Glu Gln Met Glu		
680	685	690
Asn Thr Gln Arg Ala Glu His Glu Glu Gly Gln Val Lys Asp Leu		
695	700	705
Leu Ala Glu Ser Arg Leu Arg Tyr Lys Asp Tyr Ile Gln Ile Leu		
710	715	720
Ser Ser Pro Asn Phe Ser Leu Asp Gln Tyr Cys Glu Gln Met Trp		
725	730	735
His Arg Glu Lys Arg Arg Gln Arg Asn Lys Gly Gly Pro Lys Trp		
740	745	750
Lys His Met Gln Glu Met Lys Lys Arg Asn Arg Arg His His		
755	760	765
Arg Asp Leu Asp Glu Leu Pro Arg Ala Val Ala Thr		
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<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-25

<223> Synthetic construct.

<400> 311

caacgcagcc gtgataaaca agtgg 25

<210> 312

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 312

gcttggacat gtaccaggcc gtgg 24

<210> 313

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 313
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<210> 314
<211> 3934
<212> DNA
<213> Homo sapiens
<400> 314
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<210> 315
<211> 370
<212> PRT
<213> Homo sapiens

<400> 315
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Val Phe Pro Pro Thr Pro Val Leu Cys Leu Pro Asn Gln Val Leu
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 35 40 45
 Pro Ser Ile Glu Gln Arg Leu Gln Glu Val Arg Glu Ser Ile Arg
 50 55 60
 Arg Ala Gln Val Ser Gln Val Lys Gly Ala Ala Arg Leu Ala Leu
 65 70 75
 Leu Gln Gly Ala Gly Leu Asp Val Glu Arg Trp Leu Lys Pro Ala
 80 85 90
 Met Thr Gln Ala Gln Asp Glu Val Glu Gln Glu Arg Arg Leu Ser
 95 100 105
 Glu Ala Arg Leu Ser Gln Arg Asp Leu Ser Pro Thr Ala Glu Asp
 110 115 120
 Ala Glu Leu Ser Asp Phe Glu Glu Cys Glu Glu Thr Gly Glu Leu
 125 130 135
 Phe Glu Glu Pro Ala Pro Gln Ala Leu Ala Thr Arg Ala Leu Pro
 140 145 150
 Cys Pro Ala His Val Val Phe Arg Tyr Gln Ala Gly Arg Glu Asp
 155 160 165
 Glu Leu Thr Ile Thr Glu Gly Glu Trp Leu Glu Val Ile Glu Glu
 170 175 180
 Gly Asp Ala Asp Glu Trp Val Lys Ala Arg Asn Gln His Gly Glu
 185 190 195
 Val Gly Phe Val Pro Glu Arg Tyr Leu Asn Phe Pro Asp Leu Ser
 200 205 210
 Leu Pro Glu Ser Ser Gln Asp Ser Asp Asn Pro Cys Gly Ala Glu
 215 220 225
 Pro Thr Ala Phe Leu Ala Gln Ala Leu Tyr Ser Tyr Thr Gly Gln
 230 235 240
 Ser Ala Glu Glu Leu Ser Phe Pro Glu Gly Ala Leu Ile Arg Leu
 245 250 255
 Leu Pro Arg Ala Gln Asp Gly Val Asp Asp Gly Phe Trp Arg Gly
 260 265 270
 Glu Phe Gly Gly Arg Val Gly Val Phe Pro Ser Leu Leu Val Glu
 275 280 285
 Glu Leu Leu Gly Pro Pro Gly Pro Pro Glu Leu Ser Asp Pro Glu
 290 295 300
 Gln Met Leu Pro Ser Pro Ser Pro Ser Phe Ser Pro Pro Ala

305	310	315
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320	325	330
Asp Lys Ala Leu Asp Phe Pro Gly Phe Leu Asp Met Met Ala Pro		
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<210> 316
<211> 4407
<212> DNA
<213> Homo sapiens

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<210> 317

<211> 837

<212> PRT

<213> Homo sapiens

<400> 317

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Leu	Ser	Trp	Leu	Val	Trp	Leu	Leu	Leu	Leu	Leu	Ala	Ser	Leu	
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Leu	Pro	Ser	Ala	Arg	Leu	Ala	Ser	Pro	Leu	Pro	Arg	Glu	Glu	
	50							55					60	
Ile	Val	Phe	Pro	Glu	Lys	Leu	Asn	Gly	Ser	Val	Leu	Pro	Gly	Ser
	65							70					75	
Gly	Ala	Pro	Ala	Arg	Leu	Leu	Cys	Arg	Leu	Gln	Ala	Phe	Gly	Glu
	80							85					90	
Thr	Leu	Leu	Leu	Glu	Leu	Glu	Gln	Asp	Ser	Gly	Val	Gln	Val	Glu
	95							100					105	
Gly	Leu	Thr	Val	Gln	Tyr	Leu	Gly	Gln	Ala	Pro	Glu	Leu	Leu	Gly
	110							115					120	
Gly	Ala	Glu	Pro	Gly	Thr	Tyr	Leu	Thr	Gly	Thr	Ile	Asn	Gly	Asp
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Pro	Glu	Ser	Val	Ala	Ser	Leu	His	Trp	Asp	Gly	Gly	Ala	Leu	Leu

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Glu Gly Gly Thr Pro Asn Ser Ala Gly	Gly Pro Gly Ala His Ile	
170	175	180
Leu Arg Arg Lys Ser Pro Ala Ser Gly	Gln Gly Pro Met Cys Asn	
185	190	195
Val Lys Ala Pro Leu Gly Ser Pro Ser	Pro Arg Pro Arg Arg Ala	
200	205	210
Lys Arg Phe Ala Ser Leu Ser Arg Phe	Val Glu Thr Leu Val Val	
215	220	225
Ala Asp Asp Lys Met Ala Ala Phe His	Gly Ala Gly Leu Lys Arg	
230	235	240
Tyr Leu Leu Thr Val Met Ala Ala Ala	Lys Ala Phe Lys His	
245	250	255
Pro Ser Ile Arg Asn Pro Val Ser Leu	Val Val Thr Arg Leu Val	
260	265	270
Ile Leu Gly Ser Gly Glu Glu Gly Pro	Gln Val Gly Pro Ser Ala	
275	280	285
Ala Gln Thr Leu Arg Ser Phe Cys Ala	Trp Gln Arg Gly Leu Asn	
290	295	300
Thr Pro Glu Asp Ser Gly Pro Asp His	Phe Asp Thr Ala Ile Leu	
305	310	315
Phe Thr Arg Gln Asp Leu Cys Gly Val	Ser Thr Cys Asp Thr Leu	
320	325	330
Gly Met Ala Asp Val Gly Thr Val Cys	Asp Pro Ala Arg Ser Cys	
335	340	345
Ala Ile Val Glu Asp Asp Gly Leu Gln	Ser Ala Phe Thr Ala Ala	
350	355	360
His Glu Leu Gly His Val Phe Asn Met	Leu His Asp Asn Ser Lys	
365	370	375
Pro Cys Ile Ser Leu Asn Gly Pro Leu	Ser Thr Ser Arg His Val	
380	385	390
Met Ala Pro Val Met Ala His Val Asp	Pro Glu Glu Pro Trp Ser	
395	400	405
Pro Cys Ser Ala Arg Phe Ile Thr Asp	Phe Leu Asp Asn Gly Tyr	
410	415	420
Gly His Cys Leu Leu Asp Lys Pro Glu	Ala Pro Leu His Leu Pro	
425	430	435

Val Thr Phe Pro Gly Lys Asp Tyr Asp Ala Asp Arg Gln Cys Gln
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 Leu Thr Phe Gly Pro Asp Ser Arg His Cys Pro Gln Leu Pro Pro
 455 460 465
 Pro Cys Ala Ala Leu Trp Cys Ser Gly His Leu Asn Gly His Ala
 470 475 480
 Met Cys Gln Thr Lys His Ser Pro Trp Ala Asp Gly Thr Pro Cys
 485 490 495
 Gly Pro Ala Gln Ala Cys Met Gly Gly Arg Cys Leu His Met Asp
 500 505 510
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 515 520 525
 Trp Gly Pro Trp Gly Asp Cys Ser Arg Thr Cys Gly Gly Val
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 Gln Phe Ser Ser Arg Asp Cys Thr Arg Pro Val Pro Arg Asn Gly
 545 550 555
 Gly Lys Tyr Cys Glu Gly Arg Arg Thr Arg Phe Arg Ser Cys Asn
 560 565 570
 Thr Glu Asp Cys Pro Thr Gly Ser Ala Leu Thr Phe Arg Glu Glu
 575 580 585
 Gln Cys Ala Ala Tyr Asn His Arg Thr Asp Leu Phe Lys Ser Phe
 590 595 600
 Pro Gly Pro Met Asp Trp Val Pro Arg Tyr Thr Gly Val Ala Pro
 605 610 615
 Gln Asp Gin Cys Lys Leu Thr Cys Gln Ala Arg Ala Leu Gly Tyr
 620 625 630
 Tyr Tyr Val Leu Glu Pro Arg Val Val Asp Gly Thr Pro Cys Ser
 635 640 645
 Pro Asp Ser Ser Ser Val Cys Val Gln Gly Arg Cys Ile His Ala
 650 655 660
 Gly Cys Asp Arg Ile Ile Gly Ser Lys Lys Lys Phe Asp Lys Cys
 665 670 675
 Met Val Cys Gly Gly Asp Gly Ser Gly Cys Ser Lys Gln Ser Gly
 680 685 690
 Ser Phe Arg Lys Phe Arg Tyr Gly Tyr Asn Asn Val Val Thr Ile
 695 700 705
 Pro Ala Gly Ala Thr His Ile Leu Val Arg Gln Gln Gly Asn Pro
 710 715 720
 Gly His Arg Ser Ile Tyr Leu Ala Leu Lys Leu Pro Asp Gly Ser

725	730	735
Tyr Ala Leu Asn Gly Glu Tyr Thr Leu Met Pro Ser Pro Thr Asp		
740	745	750
Val Val Leu Pro Gly Ala Val Ser Leu Arg Tyr Ser Gly Ala Thr		
755	760	765
Ala Ala Ser Glu Thr Leu Ser Gly His Gly Pro Leu Ala Gln Pro		
770	775	780
Leu Thr Leu Gln Val Leu Val Ala Gly Asn Pro Gln Asp Thr Arg		
785	790	795
Leu Arg Tyr Ser Phe Phe Val Pro Arg Pro Thr Pro Ser Thr Pro		
800	805	810
Arg Pro Thr Pro Gln Asp Trp Leu His Arg Arg Ala Gln Ile Leu		
815	820	825
Glu Ile Leu Arg Arg Arg Pro Trp Ala Gly Arg Lys		
830	835	

<210> 318
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 318
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<210> 319
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 319
cttgctctt cggcgcgccc agtc 24

<210> 320
<211> 43
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-43
<223> Synthetic construct.

<400> 320
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<210> 321
<211> 1197
<212> DNA
<213> Homo sapiens

<400> 321
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tttgtggactg gtgtttggta tcctggccct aactctaatt gtcctgttt 200
gggggagcaa gcacttctgg ccggaggtagc ccaaaaaagc ctatgacatg 250
gagcacactt tctacagcaa tggagagaag aagaagattt acatggaaat 300
tgatcctgtg accagaactg aaatattcag aagcgaaat ggcactgatg 350
aacatggaa agtgcacgac tttaaaaacg gatacactgg catctacttc 400
gtgggtcttc aaaaatgttt tatcaaaact cagattaaag tgattcctga 450
atttctgaa ccagaagagg aaatagatga gaatgaagaa attaccacaa 500
ctttcttga acagtcagtg atttgggtcc cagcagaaaa gcctattgaa 550
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gaccatgtat tggatcaatc ccactctaatt atcagttct gagttacaag 650
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gaccgcgtcac gccagacaag caagtgagga agaacttcca ataaatgact 800
atactgaaaaa tggaaatagaa tttgatccca tgctggatga gagaggttat 850
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acctttacta ggctactacc catatccata ctgctaccaa ggaggacgag 950
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<210> 322

<211> 317

<212> PRT

<213> Homo sapiens

<400> 322

Met	Ala	Lys	Asn	Pro	Pro	Glu	Asn	Cys	Glu	Asp	Cys	His	Ile	Leu	
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Asn	Ala	Glu	Ala	Phe	Lys	Ser	Lys	Lys	Ile	Cys	Lys	Ser	Leu	Lys	
		20						25							30
Ile	Cys	Gly	Leu	Val	Phe	Gly	Ile	Leu	Ala	Leu	Thr	Leu	Ile	Val	
			35					40							45
Leu	Phe	Trp	Gly	Ser	Lys	His	Phe	Trp	Pro	Glu	Val	Pro	Lys	Lys	
				50				55							60
Ala	Tyr	Asp	Met	Glu	His	Thr	Phe	Tyr	Ser	Asn	Gly	Glu	Lys	Lys	
			65					70							75
Lys	Ile	Tyr	Met	Glu	Ile	Asp	Pro	Val	Thr	Arg	Thr	Glu	Ile	Phe	
			80					85							90
Arg	Ser	Gly	Asn	Gly	Thr	Asp	Glu	Thr	Leu	Glu	Val	His	Asp	Phe	
			95					100							105
Lys	Asn	Gly	Tyr	Thr	Gly	Ile	Tyr	Phe	Val	Gly	Leu	Gln	Lys	Cys	
			110					115							120
Phe	Ile	Lys	Thr	Gln	Ile	Lys	Val	Ile	Pro	Glu	Phe	Ser	Glu	Pro	
			125					130							135
Glu	Glu	Glu	Ile	Asp	Glu	Asn	Glu	Glu	Ile	Thr	Thr	Thr	Phe	Phe	
			140					145							150
Glu	Gln	Ser	Val	Ile	Trp	Val	Pro	Ala	Glu	Lys	Pro	Ile	Glu	Asn	
			155					160							165
Arg	Asp	Phe	Leu	Lys	Asn	Ser	Lys	Ile	Leu	Glu	Ile	Cys	Asp	Asn	
			170					175							180
Val	Thr	Met	Tyr	Trp	Ile	Asn	Pro	Thr	Leu	Ile	Ser	Val	Ser	Glu	
			185					190							195
Leu	Gln	Asp	Phe	Glu	Glu	Gly	Glu	Asp	Leu	His	Phe	Pro	Ala		
			200					205							210
Asn	Glu	Lys	Lys	Gly	Ile	Glu	Gln	Asn	Glu	Gln	Trp	Val	Val	Pro	
			215					220							225
Gln	Val	Lys	Val	Glu	Lys	Thr	Arg	His	Ala	Arg	Gln	Ala	Ser	Glu	
			230					235							240
Glu	Glu	Leu	Pro	Ile	Asn	Asp	Tyr	Thr	Glu	Asn	Gly	Ile	Glu	Phe	
			245					250							255
Asp	Pro	Met	Leu	Asp	Glu	Arg	Gly	Tyr	Cys	Cys	Ile	Tyr	Cys	Arg	
			260					265							270

Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly
275 280 285

Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys
290 295 300

Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly
305 310 315

Arg Val

<210> 323

<211> 1174

<212> DNA

<213> Homo sapiens

<400> 323

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ggccgtgcag cttctggct tcctgctcag cttcctggc atggtggca 150
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accaacatcc tcacggccgt gtcctacctg aaagggtctt ggatggagt 250
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<210> 324

<211> 239

<212> PRT

<213> Homo sapiens

<400> 324

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Leu	Gly	Met	Val	Gly	Thr	Leu	Ile	Thr	Thr	Ile	Leu	Pro	His	Trp
			20					25				30		
Arg	Arg	Thr	Ala	His	Val	Gly	Thr	Asn	Ile	Leu	Thr	Ala	Val	Ser
				35				40				45		
Tyr	Leu	Lys	Gly	Leu	Trp	Met	Glu	Cys	Val	Trp	His	Ser	Thr	Gly
				50				55			60			
Ile	Tyr	Gln	Cys	Gln	Ile	Tyr	Arg	Ser	Leu	Leu	Ala	Leu	Pro	Gln
				65				70			75			
Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Met	Val	Ile	Ser	Cys	Leu	Leu
				80				85			90			
Ser	Gly	Ile	Ala	Cys	Ala	Cys	Ala	Val	Ile	Gly	Met	Lys	Cys	Thr
				95				100			105			
Arg	Cys	Ala	Lys	Gly	Thr	Pro	Ala	Lys	Thr	Thr	Phe	Ala	Ile	Leu
				110				115			120			
Gly	Gly	Thr	Leu	Phe	Ile	Leu	Ala	Gly	Leu	Leu	Cys	Met	Val	Ala
				125				130			135			
Val	Ser	Trp	Thr	Thr	Asn	Asp	Val	Val	Gln	A&nbsn	Phe	Tyr	Asn	Pro
				140				145			150			
Leu	Leu	Pro	Ser	Gly	Met	Lys	Phe	Glu	Ile	Gly	Gln	Ala	Leu	Tyr
				155				160			165			
Leu	Gly	Phe	Ile	Ser	Ser	Ser	Leu	Ser	Leu	Ile	Gly	Gly	Thr	Leu
				170				175			180			
Leu	Cys	Leu	Ser	Cys	Gln	Asp	Glu	Ala	Pro	Tyr	Arg	Pro	Tyr	Gln
				185				190			195			
Ala	Pro	Pro	Arg	Ala	Thr	Thr	Thr	Ala	Asn	Thr	Ala	Pro	Ala	
				200				205			210			
Tyr	Gln	Pro	Pro	Ala	Ala	Tyr	Lys	Asp	Asn	Arg	Ala	Pro	Ser	Val
				215				220			225			

Thr Ser Ala Thr His Ser Gly Tyr Arg Leu Asn Asp Tyr Val
230 235

<210> 325

<211> 2121

<212> DNA

<213> Homo sapiens

<400> 325

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<210> 326

<211> 261

<212> PRT

<213> Homo sapiens

<400> 326

Met	Ser	Thr	Thr	Thr	Cys	Gln	Val	Val	Ala	Phe	Leu	Leu	Ser	Ile
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Leu	Gly	Leu	Ala	Gly	Cys	Ile	Ala	Ala	Thr	Gly	Met	Asp	Met	Trp
20									25					30

Ser	Thr	Gln	Asp	Leu	Tyr	Asp	Asn	Pro	Val	Thr	Ser	Val	Phe	Gln
										35				45

Tyr	Glu	Gly	Leu	Trp	Arg	Ser	Cys	Val	Arg	Gln	Ser	Ser	Gly	Phe
									55					60

Thr	Glu	Cys	Arg	Pro	Tyr	Phe	Thr	Ile	Leu	Gly	Leu	Pro	Ala	Met
								65						75

Leu Gln Ala Val Arg Ala Leu Met Ile Val Gly Ile Val Leu Gly

80	85	90
Ala Ile Gly Leu Leu Val Ser Ile Phe Ala Leu Lys Cys Ile Arg		
95	100	105
Ile Gly Ser Met Glu Asp Ser Ala Lys Ala Asn Met Thr Leu Thr		
110	115	120
Ser Gly Ile Met Phe Ile Val Ser Gly Leu Cys Ala Ile Ala Gly		
125	130	135
Val Ser Val Phe Ala Asn Met Leu Val Thr Asn Phe Trp Met Ser		
140	145	150
Thr Ala Asn Met Tyr Thr Gly Met Gly Met Val Gln Thr Val		
155	160	165
Gln Thr Arg Tyr Thr Phe Gly Ala Ala Leu Phe Val Gly Trp Val		
170	175	180
Ala Gly Gly Leu Thr Leu Ile Gly Gly Val Met Met Cys Ile Ala		
185	190	195
Cys Arg Gly Leu Ala Pro Glu Glu Thr Asn Tyr Lys Ala Val Ser		
200	205	210
Tyr His Ala Ser Gly His Ser Val Ala Tyr Lys Pro Gly Gly Phe		
215	220	225
Lys Ala Ser Thr Gly Phe Gly Ser Asn Thr Lys Asn Lys Lys Ile		
230	235	240
Tyr Asp Gly Gly Ala Arg Thr Glu Asp Glu Val Gln Ser Tyr Pro		
245	250	255
Ser Lys His Asp Tyr Val		
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<210> 327

<211> 2010

<212> DNA

<213> Homo sapiens

<400> 327

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ctgctgacgg ctgaaatcat cttcatcatc acggcatgg tggtgctcat 500
ccctgtgagc tgggtgcca atgccatcat cagagattc tataactcaa 550
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 <210> 328
 <211> 225
 <212> PRT
 <213> Homo sapiens

 <400> 328
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 35 40 45
 Phe Trp Glu Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile
 50 55 60
 Arg Met Gln Cys Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro
 65 70 75
 Asp Leu Gln Ala Ala Arg Gly Leu Met Cys Ala Ala Ser Val Met
 80 85 90
 Ser Phe Leu Ala Phe Met Met Ala Ile Leu Gly Met Lys Cys Thr
 95 100 105
 Arg Cys Thr Gly Asp Asn Glu Lys Val Lys Ala His Ile Leu Leu
 110 115 120
 Thr Ala Gly Ile Ile Phe Ile Ile Thr Gly Met Val Val Leu Ile
 125 130 135
 Pro Val Ser Trp Val Ala Asn Ala Ile Ile Arg Asp Phe Tyr Asn
 140 145 150
 Ser Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly Glu Ala Leu
 155 160 165
 Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile Val Gly Gly Ala
 170 175 180
 Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser Ser Ser Tyr
 185 190 195
 Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser Tyr His
 200 205 210

Thr Gly Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr Val
215 220 225

<210> 329

<211> 1315

<212> DNA

<213> Homo sapiens

<400> 329

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cagctatgtt gaccccgcc cccacctcca acactgcacc cttctgccct 1250

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tgttttgtta gtgca 1315

<210> 330

<211> 220

<212> PRT

<213> Homo sapiens

<400> 330

Met Ala Ser Ala Gly Met Gln Ile Leu Gly Val Val Leu Thr Leu
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Leu Gly Trp Val Asn Gly Leu Val Ser Cys Ala Leu Pro Met Trp
20 25 30

Lys Val Thr Ala Phe Ile Gly Asn Ser Ile Val Val Ala Gln Val
35 40 45

Val Trp Glu Gly Leu Trp Met Ser Cys Val Val Gln Ser Thr Gly
50 55 60

Gln Met Gln Cys Lys Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln
65 70 75

Asp Leu Gln Ala Ala Arg Ala Leu Cys Val Ile Ala Leu Leu Val
80 85 90

Ala Leu Phe Gly Leu Leu Val Tyr Leu Ala Gly Ala Lys Cys Thr
95 100 105

Thr Cys Val Glu Glu Lys Asp Ser Lys Ala Arg Leu Val Leu Thr
110 115 120

Ser Gly Ile Val Phe Val Ile Ser Gly Val Leu Thr Leu Ile Pro
125 130 135

Val Cys Trp Thr Ala His Ala Ile Ile Arg Asp Phe Tyr Asn Pro
140 145 150

Leu Val Ala Glu Ala Gln Lys Arg Glu Leu Gly Ala Ser Leu Tyr
155 160 165

Leu Gly Trp Ala Ala Ser Gly Leu Leu Leu Gly Gly Gly Leu
170 175 180

Leu Cys Cys Thr Cys Pro Ser Gly Gly Ser Gln Gly Pro Ser His
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Tyr Met Ala Arg Tyr Ser Thr Ser Ala Pro Ala Ile Ser Arg Gly
200 205 210

Pro Ser Glu Tyr Pro Thr Lys Asn Tyr Val
215 220

<210> 331

<211> 1160

<212> DNA

<213> Homo sapiens

<400> 331
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gttccttggc atggtggga ctcttgccac aacccttctg cctcagtgg 200
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caagtgtaca atgatggact acttattact tttgaccat catgtattat 1100
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<210> 332

<211> 173

<212> PRT

<213> Homo sapiens

<400> 332

Met Asn Cys Ile Arg Gln Ala Arg Val Arg Leu Gln Cys Lys Phe

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			20			25			30					
Ala	Leu	Met	Cys	Val	Ala	Val	Ala	Leu	Ser	Leu	Ile	Ala	Leu	Leu
	35				35			40			45			
Ile	Gly	Ile	Cys	Gly	Met	Lys	Gln	Val	Gln	Cys	Thr	Gly	Ser	Asn
		50				55			60					
Glu	Arg	Ala	Lys	Ala	Tyr	Leu	Leu	Gly	Thr	Ser	Gly	Val	Leu	Phe
		65				70			75					
Ile	Leu	Thr	Gly	Ile	Phe	Val	Leu	Ile	Pro	Val	Ser	Trp	Thr	Ala
		80					85					90		
Asn	Ile	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	Pro	Ala	Ile	His	Ile	Gly
		95						100				105		
Gln	Lys	Arg	Glu	Leu	Gly	Ala	Ala	Leu	Phe	Leu	Gly	Trp	Ala	Ser
		110						115				120		
Ala	Ala	Val	Leu	Phe	Ile	Gly	Gly	Leu	Leu	Cys	Gly	Phe	Cys	
		125					130					135		
Cys	Cys	Asn	Arg	Lys	Lys	Gln	Gly	Tyr	Arg	Tyr	Pro	Val	Pro	Gly
		140						145				150		
Tyr	Arg	Val	Pro	His	Thr	Asp	Lys	Arg	Arg	Asn	Thr	Thr	Met	Leu
		155						160				165		
Ser	Lys	Thr	Ser	Thr	Ser	Tyr	Val							
		170												
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ctcagaagct	gctagtctgt	ctccaaaaaa	agtggactgc	agcatttaca	150									
agaagtatcc	agtggtgcc	atcccctgcc	ccatcacata	cctaccagg	200									
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gagcttgaaa	agtaatggaa	gagttcagtt	tcttcacgat	ggaagttgct	300									
aaattctcca	tggacataga	gagaaaggaa	tgatattctc	atcatcatct	350									
tcatcatccc	aggctctgac	tgagttctt	tcagtttac	tgatgttctg	400									
ggtgggggac	agagccagat	tcagagtaat	cttgactgaa	tggagaaaagt	450									

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 ttttaaacac gtcaataaaa aaataatctc ccaga 535
 <210> 334
 <211> 85
 <212> PRT
 <213> Homo sapiens
 <400> 334
 Met Lys Ile Thr Gly Gly Leu Leu Leu Leu Cys Thr Val Val Tyr
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 Phe Cys Ser Ser Glu Ala Ala Ser Leu Ser Pro Lys Lys Val
 20 25 30
 Asp Cys Ser Ile Tyr Lys Lys Tyr Pro Val Val Ala Ile Pro Cys
 35 40 45
 Pro Ile Thr Tyr Leu Pro Val Cys Gly Ser Asp Tyr Ile Thr Tyr
 50 55 60
 Gly Asn Glu Cys His Leu Cys Thr Glu Ser Leu Lys Ser Asn Gly
 65 70 75
 Arg Val Gln Phe Leu His Asp Gly Ser Cys
 80 85
 <210> 335
 <211> 742
 <212> DNA
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 <210> 336
 <211> 148
 <212> PRT
 <213> Homo sapiens
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 20 25 30
 Gly Asn Lys Leu Lys Leu Met Leu Gln Lys Arg Glu Ala Pro Val
 35 40 45
 Pro Thr Lys Thr Lys Val Ala Val Asp Glu Asn Lys Ala Lys Glu
 50 55 60
 Phe Leu Gly Ser Leu Lys Arg Gln Lys Arg Gln Leu Trp Asp Arg
 65 70 75
 Thr Arg Pro Glu Val Gln Gln Trp Tyr Gln Gln Phe Leu Tyr Met
 80 85 90
 Gly Phe Asp Glu Ala Lys Phe Glu Asp Asp Ile Thr Tyr Trp Leu
 95 100 105
 Asn Arg Asp Arg Asn Gly His Glu Tyr Tyr Gly Asp Tyr Tyr Gln
 110 115 120
 Arg His Tyr Asp Glu Asp Ser Ala Ile Gly Pro Arg Ser Pro Tyr
 125 130 135
 Gly Phe Arg His Gly Ala Ser Val Asn Tyr Asp Asp Tyr
 140 145 145
 <210> 337
 <211> 1310
 <212> DNA
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 tgaaggggtg ggtgatgagg tgaccgtcct tttctcggtg cttgcctgcc 150
 ttctggtgct ggcccttgcc tgggtctcaa cgcacaccgc tgagggcggg 200
 gaccactgc cccagccgtc agggacccca acgccatccc agcccagcgc 250

agccatggca gctaccgaca gcatgagagg ggaggccccca ggggcagaga 300
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cctgctgttg ctgctgctct ggtactgcca gatccagtac cggcccttct 750
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ctcctggcct ttgccatgta ccgcccgtag tgcctccggc ggcgcttggc 850
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<210> 338
<211> 246
<212> PRT
<213> Homo sapiens

<400> 338
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20 25 30
Thr His Thr Ala Glu Gly Gly Asp Pro Leu Pro Gln Pro Ser Gly
35 40 45

Thr	Pro	Thr	Pro	Ser	Gln	Pro	Ser	Ala	Ala	Met	Ala	Ala	Thr	Asp
								50		55			60	
Ser	Met	Arg	Gly	Glu	Ala	Pro	Gly	Ala	Glu	Thr	Pro	Ser	Leu	Arg
								65		70			75	
His	Arg	Gly	Gln	Ala	Ala	Gln	Pro	Glu	Pro	Ser	Thr	Gly	Phe	Thr
								80		85			90	
Ala	Thr	Pro	Pro	Ala	Pro	Asp	Ser	Pro	Gln	Glu	Pro	Leu	Val	Leu
								95		100			105	
Arg	Leu	Lys	Phe	Leu	Asn	Asp	Ser	Glu	Gln	Val	Ala	Arg	Ala	Trp
								110		115			120	
Pro	His	Asp	Thr	Ile	Gly	Ser	Leu	Lys	Arg	Thr	Gln	Phe	Pro	Gly
								125		130			135	
Arg	Glu	Gln	Gln	Val	Arg	Leu	Ile	Tyr	Gln	Gly	Gln	Leu	Leu	Gly
								140		145			150	
Asp	Asp	Thr	Gln	Thr	Leu	Gly	Ser	Leu	His	Leu	Pro	Pro	Asn	Cys
								155		160			165	
Val	Leu	His	Cys	His	Val	Ser	Thr	Arg	Val	Gly	Pro	Pro	Asn	Pro
								170		175			180	
Pro	Cys	Pro	Pro	Gly	Ser	Glu	Pro	Gly	Pro	Ser	Gly	Leu	Glu	Ile
								185		190			195	
Gly	Ser	Leu	Leu	Leu	Pro	Leu								
								200		205			210	
Trp	Tyr	Cys	Gln	Ile	Gln	Tyr	Arg	Pro	Phe	Phe	Pro	Leu	Thr	Ala
								215		220			225	
Thr	Leu	Gly	Leu	Ala	Gly	Phe	Thr	Leu	Leu	Leu	Ser	Leu	Leu	Ala
								230		235			240	
Phe	Ala	Met	Tyr	Arg	Pro									
					245									

<210> 339

<211> 849

<212> DNA

<213> Homo sapiens

<400> 339

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atgacaaagg cgctactcat ctatggtc agcagtttc ttgccctaaa 200

tcaggccagc ctcatcagtc gctgtgactt ggcccaggtg ctgcagctgg 250

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<210> 340

<211> 148

<212> PRT

<213> Homo sapiens

<400> 340

Met	Thr	Lys	Ala	Leu	Leu	Ile	Tyr	Leu	Val	Ser	Ser	Phe	Leu	Ala
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Leu	Asn	Gln	Ala	Ser	Leu	Ile	Ser	Arg	Cys	Asp	Leu	Ala	Gln	Val
					20				25					30

Leu	Gln	Leu	Glu	Asp	Leu	Asp	Gly	Phe	Glu	Gly	Tyr	Ser	Leu	Ser
					35				40					45

Asp	Trp	Leu	Cys	Leu	Ala	Phe	Val	Glu	Ser	Lys	Phe	Asn	Ile	Ser
					50				55					60

Lys	Ile	Asn	Glu	Asn	Ala	Asp	Gly	Ser	Phe	Asp	Tyr	Gly	Leu	Phe
					65				70					75

Gln	Ile	Asn	Ser	His	Tyr	Trp	Cys	Asn	Asp	Tyr	Lys	Ser	Tyr	Ser
					80				85					90

Glu	Asn	Leu	Cys	His	Val	Asp	Cys	Gln	Asp	Leu	Leu	Asn	Pro	Asn
					95				100					105

Leu	Leu	Ala	Gly	Ile	His	Cys	Ala	Lys	Arg	Ile	Val	Ser	Gly	Ala
				110					115					120

Arg	Gly	Met	Asn	Asn	Trp	Val	Glu	Trp	Arg	Leu	His	Cys	Ser	Gly
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Arg Pro Leu Ser Tyr Trp Leu Thr Gly Cys Arg Leu Arg

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<210> 341
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 341
ccctccaagg atgacaaagg cgc 23

<210> 342
<211> 29
<212> DNA
<213> Artificial

<220>
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<222> 1-29
<223> Synthetic construct.

<400> 342
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<210> 343
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<213> Artificial

<220>
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<222> 1-24
<223> Synthetic construct.

<400> 343
atctcaggcg gcattctgtc agcc 24

<210> 344
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 344
gtggatgcct gcaagaaggt tggg 24

<210> 345
<211> 45
<212> DNA
<213> Artificial

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<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 345
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<210> 346
<211> 2575
<212> DNA
<213> Homo sapiens

<400> 346
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aaggagaaaa ccggggtaaa gggagggaaag caattcaatt tgaagtccct 200
gtgaatgggc tttcagaagg caattaaaga aatccactca gagaggactt 250
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<210> 347

<211> 639

<212> PRT

<213> Homo sapiens

<400> 347

Met Leu Leu Arg Lys Arg Tyr Arg His Arg Pro Cys Arg Leu Gln
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Phe Leu Leu Leu Leu Met Leu Gly Cys Val Leu Met Met Val
20 25 30

Ala Met Leu His Pro Pro His His Thr Leu His Gln Thr Val Thr
35 40 45

Ala Gln Ala Ser Lys His Ser Pro Glu Ala Arg Tyr Arg Leu Asp
50 55 60

Phe Gly Glu Ser Gln Asp Trp Val Leu Glu Ala Glu Asp Glu Gly
65 70 75

Glu Glu Tyr Ser Pro Leu Glu Gly Leu Pro Pro Phe Ile Ser Leu
80 85 90

Arg Glu Asp Gln Leu Leu Val Ala Val Ala Leu Pro Gln Ala Arg
95 100 105

Arg Asn Gln Ser Gln Gly Arg Arg Gly Ser Tyr Arg Leu Ile
110 115 120

Lys Gln Pro Arg Arg Gln Asp Lys Glu Ala Pro Lys Arg Asp Trp
125 130 135

Gly Ala Asp Glu Asp Gly Glu Val Ser Glu Glu Glu Leu Thr
140 145 150

Pro Phe Ser Leu Asp Pro Arg Gly Leu Gln Glu Ala Leu Ser Ala
155 160 165

Arg Ile Pro Leu Gln Arg Ala Leu Pro Glu Val Arg His Pro Leu
170 175 180

Cys Leu Gln Gln His Pro Gln Asp Ser Leu Pro Thr Ala Ser Val
185 190 195

Ile Leu Cys Phe His Asp Glu Ala Trp Ser Thr Leu Leu Arg Thr
200 205 210

Val His Ser Ile Leu Asp Thr Val Pro Arg Ala Phe Leu Lys Glu
215 220 225

Ile Ile Leu Val Asp Asp Leu Ser Gln Gln Gly Gln Leu Lys Ser
230 235 240

Ala Leu Ser Glu Tyr Val Ala Arg Leu Glu Gly Val Lys Leu Leu
245 250 255

Arg Ser Asn Lys Arg Leu Gly Ala Ile Arg Ala Arg Met Leu Gly
 260 265 270
 Ala Thr Arg Ala Thr Gly Asp Val Leu Val Phe Met Asp Ala His
 275 280 285
 Cys Glu Cys His Pro Gly Trp Leu Glu Pro Leu Leu Ser Arg Ile
 290 295 300
 Ala Gly Asp Arg Ser Arg Val Val Ser Pro Val Ile Asp Val Ile
 305 310 315
 Asp Trp Lys Thr Phe Gln Tyr Tyr Pro Ser Lys Asp Leu Gln Arg
 320 325 330
 Gly Val Leu Asp Trp Lys Leu Asp Phe His Trp Glu Pro Leu Pro
 335 340 345
 Glu His Val Arg Lys Ala Leu Gln Ser Pro Ile Ser Pro Ile Arg
 350 355 360
 Ser Pro Val Val Pro Gly Glu Val Val Ala Met Asp Arg His Tyr
 365 370 375
 Phe Gln Asn Thr Gly Ala Tyr Asp Ser Leu Met Ser Leu Arg Gly
 380 385 390
 Gly Glu Asn Leu Glu Leu Ser Phe Lys Ala Trp Leu Cys Gly Gly
 395 400 405
 Ser Val Glu Ile Leu Pro Cys Ser Arg Val Gly His Ile Tyr Gln
 410 415 420
 Asn Gln Asp Ser His Ser Pro Leu Asp Gln Glu Ala Thr Leu Arg
 425 430 435
 Asn Arg Val Arg Ile Ala Glu Thr Trp Leu Gly Ser Phe Lys Glu
 440 445 450
 Thr Phe Tyr Lys His Ser Pro Glu Ala Phe Ser Leu Ser Lys Ala
 455 460 465
 Glu Lys Pro Asp Cys Met Glu Arg Leu Gln Leu Gln Arg Arg Leu
 470 475 480
 Gly Cys Arg Thr Phe His Trp Phe Leu Ala Asn Val Tyr Pro Glu
 485 490 495
 Leu Tyr Pro Ser Glu Pro Arg Pro Ser Phe Ser Gly Lys Leu His
 500 505 510
 Asn Thr Gly Leu Gly Leu Cys Ala Asp Cys Gln Ala Glu Gly Asp
 515 520 525
 Ile Leu Gly Cys Pro Met Val Leu Ala Pro Cys Ser Asp Ser Arg
 530 535 540
 Gln Gln Gln Tyr Leu Gln His Thr Ser Arg Lys Glu Ile His Phe

545	550	555
Gly Ser Pro Gln His Leu Cys Phe Ala Val Arg Gln Glu Gln Val		
560	565	570
Ile Leu Gln Asn Cys Thr Glu Glu Gly Leu Ala Ile His Gln Gln		
575	580	585
His Trp Asp Phe Gln Glu Asn Gly Met Ile Val His Ile Leu Ser		
590	595	600
Gly Lys Cys Met Glu Ala Val Val Gln Glu Asn Asn Lys Asp Leu		
605	610	615
Tyr Leu Arg Pro Cys Asp Gly Lys Ala Arg Gln Gln Trp Arg Phe		
620	625	630
Asp Gln Ile Asn Ala Val Asp Glu Arg		
635		

<210> 348
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 348
ggagagggtgg tggccatgga cag 23

<210> 349
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 349
ctgtcactgc aaggagccaa cacc 24

<210> 350
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 350
tatgtcgctg cgaggtggtg aaaacctcga actgtcttc aaggc 45

<210> 351
<211> 2524
<212> DNA
<213> Homo sapiens

<400> 351
cgccaagcat gcagtaaagg ctgaaaatct gggcacagc tgaggaagac 50
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tccctctctg gccactgctg ttgctgcccc tcccaccgcc tgctcaggc 150
tcttcatcct cccctcgaac cccaccagcc ccagcccgcc ccccgtgtc 200
caggggaggc ccctcgccccc cacgtcatgt gtgcgtgtgg gagcgagcac 250
ctccaccaag ccgatctcct cgggtcccaa gatcacgtcg gcaagtccctg 300
cctggcactg caccccccagc caccccatca ggcttgagg agggccgccc 350
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tcaaataaaatg ctttgcaag ataa 2524

<210> 352

<211> 243

<212> PRT

<213> Homo sapiens

<400> 352

Met	Arg	Pro	Gln	Gly	Pro	Ala	Ala	Ser	Pro	Gln	Arg	Ileu	Arg	Gly
1					5				10				15	

Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala
 20 25 30
 Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg
 35 40 45
 Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala
 50 55 60
 Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro
 65 70 75
 Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys
 80 85 90
 Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn
 95 100 105
 Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu
 110 115 120
 Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser
 125 130 135
 Ala Leu Arg Val Leu Phe Ser Gly Ser Leu Arg Leu Lys Cys Arg
 140 145 150
 Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr Phe Asn Gly Ala Glu
 155 160 165
 Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile Tyr Leu Asp Gln
 170 175 180
 Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His Arg Thr Ser
 185 190 195
 Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu Val Asp
 200 205 210
 Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly Asp
 215 220 225
 Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu
 230 235 240
 Leu Pro Lys

<210> 353
 <211> 480
 <212> DNA
 <213> Homo sapiens

<400> 353
 gttaaccagc gcagtccctcc gtgcgtcccc cccgcccgtg ccctcactcc 50
 cggccaggat ggcattcctgt ctggccctgc gcatggcgct gctgctggtc 100

tccggggttc tggccctgc ggtgctcaca gacgatgttc cacaggagcc 150
cgtgccacg ctgtggaacg agccggccga gctgccgtcg ggagaaggcc 200
ccgtggagag caccagcccc ggccgggagc ccgtggacac cggtccccca 250
gcccccacgg tcgcgccagg acccgaggac agcaccgcgc aggagcggt 300
ggaccagggc ggccgggtcg tggggccccc cgctatcgcg gccatcgta 350
tcgcccgcct gctggccacc tgcgtggtc tggcgctcg gtgcgtcg 400
ctgagaaagt ttctgcctc ctgaagcgaa taaaggggcc gcgcggcc 450
gcggcgcgac tcggcaaaaa aaaaaaaaaa 480

<210> 354

<211> 121

<212> PRT

<213> Homo sapiens

<400> 354

Met Ala Ser Cys Leu Ala Leu Arg Met Ala Leu Leu Leu Val Ser
1 5 10 15

Gly Val Leu Ala Pro Ala Val Leu Thr Asp Asp Val Pro Gln Glu
20 25 30

Pro Val Pro Thr Leu Trp Asn Glu Pro Ala Glu Leu Pro Ser Gly
35 40 45

Glu Gly Pro Val Glu Ser Thr Ser Pro Gly Arg Glu Pro Val Asp
50 55 60

Thr Gly Pro Pro Ala Pro Thr Val Ala Pro Gly Pro Glu Asp Ser
65 70 75

Thr Ala Gln Glu Arg Leu Asp Gln Gly Gly Ser Leu Gly Pro
80 85 90

Gly Ala Ile Ala Ala Ile Val Ile Ala Ala Leu Leu Ala Thr Cys
95 100 105

Val Val Leu Ala Leu Val Val Ala Leu Arg Lys Phe Ser Ala
110 115 120

Ser

<210> 355

<211> 2134

<212> DNA

<213> Homo sapiens

<400> 355

ggccgttgtt tggtgcgccgg ctgaagggtg tggcgcgagc agcgtcggt 50

gttggccggc ggccggccgg gacgggcatg gccctgctgc tgtgccttgt 100

gtgcctgacg gcggcgctgg cccacggctg tctgcactgc cacagcaact 150
tctccaagaa gttctcccttc taccgccacc atgtgaactt caagtccctgg 200
tgggtggcgc acatccccgt gtcagggcgc ctgctcacccg actggagcga 250
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agaagctgga ccaagtggcgc acagcagtgt accagatgtat ggatcagctg 350
taccagggga agatgtactt ccccggtat ttccccaaacg agctgcgaaa 400
catcttccgg gagcaggtgc acctcatcca gaacgccatc atcgaaaggc 450
acctggcacc aggcaagctgg ggaggaggc agctctccag ggagggaccc 500
agcctagcac ctgaaggatc aatgccatca ccccgcgaaa acctccccta 550
atgtagcccc agaggcgctg ggagtgtgc caccggccctc ccctgaagtt 600
tgctccatct cacgctgggg gtcaacctgg ggaccggcttc cctccggggc 650
atggacacac atacatgaaa accaggccgc atcgactgtc agcaccgctg 700
tggcatcttc cagtacgaga ccatctcctg caacaactgc acagactcgc 750
acgtcgccctg cttggctat aactgcgagt agggctcagg catcacaccc 800
acccgtgcca gggccctact gtccctgggg tcccaggctc tccttgagg 850
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ttcagggcgc caccattcc aaggctgtgt cccacaggctc ctcggcgcag 950
tggaaagtcaag ctgtcccgagg cctcctgaac tacataaata actggcacaa 1000
gtaaagtcccc tcctcaaacc aacacaggca gtgtgtgtat gtgagcacct 1050
cgtgggtgag tatgtgtggg gcacaggctg gtccttcag ctcccacgtc 1100
ctagaggggc tcccgaggag gtggAACCTC aaccCAGCTC tgCgcaggag 1150
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cgggcattt tcctaaagggt tccccataagg gtctgggttcc accccatccc 1250
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agaggaggggg ggcttaggggg tcctctagat cagtgggggc actgcaggtg 1450
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cctgggacac acagagccac cccggccttg tgagtgaccc agagaaggga 1600
ggcctcgga gaagggtgc tcgtaagcca acaccagcgt gcccggcct 1650
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cgaccggga cagagctgag ctggccaggg ccaggaggc gggagggagg 2050
gaatgggggt gggctgtgcg cagcatcagc gcctggcagag gtccgcagag 2100
ctgcggatg tgattaaagt ccctgatgtt tctc 2134

<210> 356

<211> 157

<212> PRT

<213> Homo sapiens

<400> 356

Met	Ala	Leu	Leu	Leu	Cys	Leu	Val	Cys	Leu	Thr	Ala	Ala	Leu	Ala
1					5				10				15	
His	Gly	Cys	Leu	His	Cys	His	Ser	Asn	Phe	Ser	Lys	Lys	Phe	Ser
									20		25		30	
Phe	Tyr	Arg	His	His	Val	Asn	Phe	Lys	Ser	Trp	Trp	Val	Gly	Asp
									35		40		45	
Ile	Pro	Val	Ser	Gly	Ala	Leu	Leu	Thr	Asp	Trp	Ser	Asp	Asp	Thr
									50		55		60	
Met	Lys	Glu	Leu	His	Leu	Ala	Ile	Pro	Ala	Lys	Ile	Thr	Arg	Glu
									65		70		75	
Lys	Leu	Asp	Gln	Val	Ala	Thr	Ala	Val	Tyr	Gln	Met	Met	Asp	Gln
									80		85		90	
Leu	Tyr	Gln	Gly	Lys	Met	Tyr	Phe	Pro	Gly	Tyr	Phe	Pro	Asn	Glu
									95		100		105	
Leu	Arg	Asn	Ile	Phe	Arg	Glu	Gln	Val	His	Leu	Ile	Gln	Asn	Ala
									110		115		120	
Ile	Ile	Glu	Arg	His	Leu	Ala	Pro	Gly	Ser	Trp	Gly	Gly	Gln	
									125		130		135	
Leu	Ser	Arg	Glu	Gly	Pro	Ser	Leu	Ala	Pro	Glu	Gly	Ser	Met	Pro

140

145

150

Ser Pro Arg Gly Asp Leu Pro
155

<210> 357

<211> 1536

<212> DNA

<213> Homo sapiens

<400> 357

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cctcttattt ctccctcacgt gtgagctggc tgcagaagtt gctgcagaag 100

ttgagaaatc ctcagatggc cctggtgctg cccaggaacc cacgtggctc 150

acagatgtcc cagctgccat ggaattcatt gctgccactg aggtggctgt 200

cataggcttc ttccaggatt tagaaatacc agcagtgcac atactccata 250

gcatggtgca aaaattccca ggcgtgtcat ttggatcatc cactgattct 300

gaggttctga cacactacaa catcactggg aacaccatct gcctctttcg 350

cctggtagac aatgaacaac tgaattttaga ggacgaagac attgaaagca 400

ttgatgccac caaatttggc cgtttcattt agatcaacag cctccacatg 450

gtgacagagt acaaccctgt gactgtgatt gggttattca acagcgtaat 500

tcagattcat ctccctctga taatgaacaa ggcctccccca gagtatgaag 550

agaacatgca cagataccag aaggcagcca agcttccca gggaaagatt 600

ctctttattt tggggacag tggatgtaaa gaaaatgggaa aggtgatatac 650

atttttcaaa ctaaaggagt ctcaactgcc agcttggca atttaccaga 700

ctctagatga cgagtggat acactgccca cagcagaagt ttccgttagag 750

catgtcaaa acttttgtga tggattccta agtggaaaat tggatgtaaa 800

aaatcgtaa tcagaaggaa agactccaaa ggtggaaactc tgacttctcc 850

tggaaactac atatggccaa gtatctactt tatgcaaagt aaaaaggcac 900

aactcaaatac tcagagacac taaacaacag gatcaactagg cctgccaacc 950

acacacacac gcacgtgcac acacgcacgc acgcgtgcac acacacacgc 1000

gcacacacac acacacacac agcttcattt cctgtcttaa aatctcggtt 1050

tctcttcttc cttttttaa atttcatatac ctcactccct atccaatttc 1100

cttcttatcg tgcattcata ctctgtaaac ccacatgtaa cacacctaga 1150

tcaaggcttt aagagactca ctgtgtatgcc tctatgaaag agaggcatc 1200

ctagagaaaat ttgttccaa tttgtcattt aatatcaagt ttgtatactg 1250
cacatgactt acacacaaca tagttcctgc tcttttaagg ttacctaagg 1300
gttgaaactc tacttcttt cataaggcaca tgtccgtctc tgactcagga 1350
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cagaagttaa aggctgtctc caagtccctg aactcagcag aaatagacca 1450
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caacctgcat aataaataaaa aggcaatcat gttata 1536

<210> 358

<211> 273

<212> PRT

<213> Homo sapiens

<400> 358

Met	Glu	Ala	Ala	Pro	Ser	Arg	Phe	Met	Phe	Leu	Leu	Phe	Leu	Leu
1				5				10				15		

Thr	Cys	Glu	Leu	Ala	Ala	Glu	Val	Ala	Ala	Glu	Val	Glu	Lys	Ser
			20					25				30		

Ser	Asp	Gly	Pro	Gly	Ala	Ala	Gln	Glu	Pro	Thr	Trp	Leu	Thr	Asp
				35				40				45		

Val	Pro	Ala	Ala	Met	Glu	Phe	Ile	Ala	Ala	Thr	Glu	Val	Ala	Val
				50				55				60		

Ile	Gly	Phe	Phe	Gln	Asp	Leu	Glu	Ile	Pro	Ala	Val	Pro	Ile	Leu
				65				70				75		

His	Ser	Met	Val	Gln	Lys	Phe	Pro	Gly	Val	Ser	Phe	Gly	Ile	Ser
				80				85				90		

Thr	Asp	Ser	Glu	Val	Leu	Thr	His	Tyr	Asn	Ile	Thr	Gly	Asn	Thr
				95				100				105		

Ile	Cys	Leu	Phe	Arg	Leu	Val	Asp	Asn	Glu	Gln	Leu	Asn	Leu	Glu
				110				115				120		

Asp	Glu	Asp	Ile	Glu	Ser	Ile	Asp	Ala	Thr	Lys	Leu	Ser	Arg	Phe
				125				130				135		

Ile	Glu	Ile	Asn	Ser	Leu	His	Met	Val	Thr	Glu	Tyr	Asn	Pro	Val
					140			145				150		

Thr	Val	Ile	Gly	Leu	Phe	Asn	Ser	Val	Ile	Gln	Ile	His	Leu	Leu
				155				160				165		

Leu	Ile	Met	Asn	Lys	Ala	Ser	Pro	Glu	Tyr	Glu	Glu	Asn	Met	His
				170				175				180		

Arg	Tyr	Gln	Lys	Ala	Ala	Lys	Leu	Phe	Gln	Gly	Lys	Ile	Leu	Phe
				185				190				195		

Ile Leu Val Asp Ser Gly Met Lys Glu Asn Gly Lys Val Ile Ser
200 205 210
Phe Phe Lys Leu Lys Glu Ser Gln Leu Pro Ala Leu Ala Ile Tyr
215 220 225
Gln Thr Leu Asp Asp Glu Trp Asp Thr Leu Pro Thr Ala Glu Val
230 235 240
Ser Val Glu His Val Gln Asn Phe Cys Asp Gly Phe Leu Ser Gly
245 250 255
Lys Leu Leu Lys Glu Asn Arg Glu Ser Glu Gly Lys Thr Pro Lys
260 265 270
Val Glu Leu

<210> 359

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 359

ccagcagtgc ccatactcca tagc 24

<210> 360

<211> 20

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-20

<223> Synthetic construct.

<400> 360

tgacgagtgg gatacactgc 20

<210> 361

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 361

gctctacgga aaccttctgct gtgg 24

<210> 362

<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 362
attccccaggc gtgtcatttg ggatcagcac tgattctgag gttctgacac 50

<210> 363
<211> 1777
<212> DNA
<213> Homo sapiens

<400> 363
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ccggcgcggg tggcggagag atcagaagcc tcttcccaa gccgagccaa 100
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agtggctgga cgatggcagc gtccgcccga gccggggcg tgattgcagc 200
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aaacgggatt acactggctg cagtagatca gagagttgt caccagttaa 800
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tccggcggac atcacagtga caagattaac aagtcagagt ctgtggtgta 950
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gaaacaaaac caaactggac tctcgtgcag aaaatgtac ccattaccac 1050
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atatgtaccc attgtttgc tgaaaaatgt ctttctttc aggtcattta 1250
caattggag atttcagaaa catttcatttc accatcattt agaaatggg 1300
tgccttaatg gagacaatag cagatcctgt agtatttcca gtagacatgg 1350
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tggaggatgg agatgctatg atgaaagcat acccagggtg gccttagca 1450
cagtatcgt accattttt tgtctgccgc ttttaaaaaa tacccattgg 1500
ctatgccact tgaaaacaat ttgagaagtt ttttgaagt ttttctcact 1550
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tttgcacctt tgaaatgtgt catatcaatt tctggattca taatagcaag 1650
attagcaaag gataaatgcc gaaggtcact tcattctgga cacagttgga 1700
tcaatactga ttaagtagaa aatccaagct ttgcttgaga actttgtaa 1750
cgtggagagt aaaaagtatc ggaaaa 1777

<210> 364

<211> 269

<212> PRT

<213> Homo sapiens

<400> 364

Met	Ala	Ala	Ser	Ala	Gly	Ala	Gly	Ala	Val	Ile	Ala	Ala	Pro	Asp
1				5					10				15	
Ser	Arg	Arg	Trp	Leu	Trp	Ser	Val	Leu	Ala	Ala	Ala	Leu	Gly	Leu
				20				25				30		
Leu	Thr	Ala	Gly	Val	Ser	Ala	Leu	Glu	Val	Tyr	Thr	Pro	Lys	Glu
				35				40				45		
Ile	Phe	Val	Ala	Asn	Gly	Thr	Gln	Gly	Lys	Leu	Thr	Cys	Lys	Phe
				50				55				60		
Lys	Ser	Thr	Ser	Thr	Thr	Gly	Gly	Leu	Thr	Ser	Val	Ser	Trp	Ser
				65				70				75		
Phe	Gln	Pro	Glu	Gly	Ala	Asp	Thr	Thr	Val	Ser	Phe	Phe	His	Tyr
				80				85				90		
Ser	Gln	Gly	Gln	Val	Tyr	Leu	Gly	Asn	Tyr	Pro	Pro	Phe	Lys	Asp
				95				100				105		

Arg Ile Ser Trp Ala Gly Asp Leu Asp Lys Lys Asp Ala Ser Ile
 110 115 120
 Asn Ile Glu Asn Met Gln Phe Ile His Asn Gly Thr Tyr Ile Cys
 125 130 135
 Asp Val Lys Asn Pro Pro Asp Ile Val Val Gln Pro Gly His Ile
 140 145 150
 Arg Leu Tyr Val Val Glu Lys Glu Asn Leu Pro Val Phe Pro Val
 155 160 165
 Trp Val Val Val Gly Ile Val Thr Ala Val Val Leu Gly Leu Thr
 170 175 180
 Leu Leu Ile Ser Met Ile Leu Ala Val Leu Tyr Arg Arg Lys Asn
 185 190 195
 Ser Lys Arg Asp Tyr Thr Gly Cys Ser Thr Ser Glu Ser Leu Ser
 200 205 210
 Pro Val Lys Gln Ala Pro Arg Lys Ser Pro Ser Asp Thr Glu Gly
 215 220 225
 Leu Val Lys Ser Leu Pro Ser Gly Ser His Gln Gly Pro Val Ile
 230 235 240
 Tyr Ala Gln Leu Asp His Ser Gly Gly His His Ser Asp Lys Ile
 245 250 255
 Asn Lys Ser Glu Ser Val Val Tyr Ala Asp Ile Arg Lys Asn
 260 265
 <210> 365
 <211> 1321
 <212> DNA
 <213> Homo sapiens
 <400> 365
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 cgggctgccc ccccccgggg cttggcctca agctgcggac gacgcggggt 100
 ccatcagcgc gccccggctgc cgcctctcg ccacggctgg gtcgggggcc 150
 tcgggctggg gctggggctg gcgctcgggg tgaagctggc aggtgggctg 200
 aggggcgcgg ccccgccca gtcccccgcg gcccccgacc ctgaggcgtc 250
 gcctctggcc gagccgccac aggagcagtc cctcgccccg tggtctccgc 300
 agaccccgcc gcccgcctgc tccaggtgtc tcgcgcagac catcgagac 350
 agccgcgacc tgctgcacag gatcaaggat gaggtgggcg caccgggcat 400
 agtggtttga gtttctgttag atggaaaaga agtctggta gaaggtttag 450
 gttatgctga tgttgagaac cgtgtaccat gtaaaccaga gacagttatg 500

cgaattgcta gcatcagcaa aagtctcacc atgggtgctc ttgccaaatt 550
gtggaaagca gggaaactgg atcttgatata tccagtacaa cattatgttc 600
ccgaattccc agaaaaagaa tatgaaggtg aaaaggtttc tgtcacaaca 650
agattactga tttcccattt aagtggatt cgtcattatg aaaaggacat 700
aaaaaaaggtg aaagaagaga aagcttataa agccttgaag atgatgaaag 750
agaatgttgc atttgagcaa gaaaaagaag gcaaaagtaa tgaaaagaat 800
gattttacta aatttaaac agagcaggag aatgaagcca aatgccggaa 850
ttcaaaacct ggcaagaaaa agaatgattt tgaacaaggc gaattataatt 900
tgagagaaaa gttgaaaat tcaattgaat ccctaagatt attaaaaat 950
gatccttgc tcttcaaacc tggtagtcag tttttgtatt caactttgg 1000
ctatacccta ctggcagcca tagtagagag agcttcagga tgtaaatatt 1050
tggactatat gcagaaaata ttccatgact tggatatgct gacgactgtg 1100
caggaagaaa acgagccagt gatttacaat agagcaaggt aaatgaatac 1150
cttctgctgt gtctagctat atcgcatctt aacactatTT tattaattaa 1200
aagtcaaatt ttcttgcgtt ccattccaaa atcaacctgc cacatTTgg 1250
gagctttct acatgtctgt tttctcatct gtaaagtgaa ggaagtaaaa 1300
catgtttata aagtaaaaaa a 1321

<210> 366

<211> 373

<212> PRT

<213> Homo sapiens

<400> 366

Met	Tyr	Arg	Leu	Leu	Ser	Ala	Val	Thr	Ala	Arg	Ala	Ala	Ala	Pro
1										10				15

Gly	Gly	Leu	Ala	Ser	Ser	Cys	Gly	Arg	Arg	Gly	Val	His	Gln	Arg
											20		25	30

Ala	Gly	Leu	Pro	Pro	Leu	Gly	His	Gly	Trp	Val	Gly	Gly	Leu	Gly
										35		40		45

Leu	Gly	Leu	Gly	Leu	Ala	Leu	Gly	Val	Lys	Leu	Ala	Gly	Gly	Leu
									50		55		60	

Arg	Gly	Ala	Ala	Pro	Ala	Gln	Ser	Pro	Ala	Ala	Pro	Asp	Pro	Glu
											65		70	75

Ala	Ser	Pro	Leu	Ala	Glu	Pro	Pro	Gln	Glu	Gln	Ser	Leu	Ala	Pro
											80		85	90

Trp	Ser	Pro	Gln	Thr	Pro	Ala	Pro	Pro	Cys	Ser	Arg	Cys	Phe	Ala
95							100						105	
Arg	Ala	Ile	Glu	Ser	Ser	Arg	Asp	Leu	Leu	His	Arg	Ile	Lys	Asp
110								115					120	
Glu	Val	Gly	Ala	Pro	Gly	Ile	Val	Val	Gly	Val	Ser	Val	Asp	Gly
125								130					135	
Lys	Glu	Val	Trp	Ser	Glu	Gly	Leu	Gly	Tyr	Ala	Asp	Val	Glu	Asn
140								145					150	
Arg	Val	Pro	Cys	Lys	Pro	Glu	Thr	Val	Met	Arg	Ile	Ala	Ser	Ile
155								160					165	
Ser	Lys	Ser	Leu	Thr	Met	Val	Ala	Leu	Ala	Lys	Leu	Trp	Glu	Ala
170								175					180	
Gly	Lys	Leu	Asp	Leu	Asp	Ile	Pro	Val	Gln	His	Tyr	Val	Pro	Glu
185								190					195	
Phe	Pro	Glu	Lys	Glu	Tyr	Glu	Gly	Glu	Lys	Val	Ser	Val	Thr	Thr
200								205					210	
Arg	Leu	Leu	Ile	Ser	His	Leu	Ser	Gly	Ile	Arg	His	Tyr	Glu	Lys
215								220					225	
Asp	Ile	Lys	Lys	Val	Lys	Glu	Glu	Lys	Ala	Tyr	Lys	Ala	Leu	Lys
230								235					240	
Met	Met	Lys	Glu	Asn	Val	Ala	Phe	Glu	Gln	Glu	Lys	Glu	Gly	Lys
245								250					255	
Ser	Asn	Glu	Lys	Asn	Asp	Phe	Thr	Lys	Phe	Lys	Thr	Glu	Gln	Glu
260								265					270	
Asn	Glu	Ala	Lys	Cys	Arg	Asn	Ser	Lys	Pro	Gly	Lys	Lys	Lys	Asn
275								280					285	
Asp	Phe	Glu	Gln	Gly	Glu	Leu	Tyr	Leu	Arg	Glu	Lys	Phe	Glu	Asn
290								295					300	
Ser	Ile	Glu	Ser	Leu	Arg	Leu	Phe	Lys	Asn	Asp	Pro	Leu	Phe	Phe
305								310					315	
Lys	Pro	Gly	Ser	Gln	Phe	Leu	Tyr	Ser	Thr	Phe	Gly	Tyr	Thr	Leu
320								325					330	
Leu	Ala	Ala	Ile	Val	Glu	Arg	Ala	Ser	Gly	Cys	Lys	Tyr	Leu	Asp
335								340					345	
Tyr	Met	Gln	Lys	Ile	Phe	His	Asp	Leu	Asp	Met	Leu	Thr	Thr	Val
350								355					360	
Gln	Glu	Glu	Asn	Glu	Pro	Val	Ile	Tyr	Asn	Arg	Ala	Arg		
365								370						

<210> 367

<211> 30
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-30
<223> Synthetic construct.

<400> 367
tggaaaagaa gtctggtcag aaggtttagg 30

<210> 368
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 368
catttgctt catttcctg ctctg 25

<210> 369
<211> 28
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-28
<223> Synthetic construct.

<400> 369
aaaaccttag aacaactcat tttgcacc 28

<210> 370
<211> 41
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-41
<223> Synthetic construct.

<400> 370
gtctcaccat ggttgcttt gccaaattgt ggaaaggcagg g 41

<210> 371
<211> 1150
<212> DNA
<213> Homo sapiens

<400> 371
gtgacactat agaagagcta tgacgtcgca tgcacgcgt a cgtaagctcg 50

/

gaattcggt cgaggctggg gggagaagc cgagatggcg gcagccagcg 100
ctggggcaac ccggctgctc ctgctctgc tggatggcggt agcagcgccc 150
agtgcagccc ggggcagcgg ctgccggcc gggactgggt cgcgaggggc 200
tggggcggaa ggtcgagagg gcgaggcctg tggcacggtg gggctgctgc 250
tggagcactc atttgagatc gatgacagtg ccaacttccg gaagcggggc 300
tcactgctct ggaaccagca ggatggtacc ttgtccctgt cacagcgca 350
gctcagcgag gaggagcggg gccgactccg ggatgtggca gccctgaatg 400
gcctgtaccc ggtccggatc ccaaggcgac ccggggccct ggatggcctg 450
gaagctggtg gctatgtctc ctccttgct cctgcgtgct ccctggtgaa 500
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gcccaccaca gccccaggcc ctgagacggc ggccttcatt gagcgcctgg 700
agatggaaca gccccagaag gccaagaacc cccaggagca gaagtccttc 750
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agcttccagc agccaaaagc aactgttggt ttggcaagac ggtcctgatg 1000
tacaagcttg attgaaattc actgctact tgatacgtta ttcagaaacc 1050
caaggaatgg ctgtccccat cctcatgtgg ctgtgtggag ctcagctgtg 1100
ttgtgtggca gtttattaaa ctgtccccca gatcgacacg caaaaaaaaaa 1150

<210> 372

<211> 269

<212> PRT

<213> Homo sapiens

<400> 372

Met	Ala	Ala	Ala	Ser	Ala	Gly	Ala	Thr	Arg	Leu	Leu	Leu	Leu	Leu
1										10				15

Leu	Met	Ala	Val	Ala	Ala	Pro	Ser	Arg	Ala	Arg	Gly	Ser	Gly	Cys
											25			30

Arg	Ala	Gly	Thr	Gly	Ala	Arg	Gly	Ala	Gly	Ala	Glu	Gly	Arg	Glu
											35			40

Gly Glu Ala Cys Gly Thr Val Gly Leu Leu Leu Glu His Ser Phe
 50 55 60

Glu Ile Asp Asp Ser Ala Asn Phe Arg Lys Arg Gly Ser Leu Leu
 65 70 75

Trp Asn Gln Gln Asp Gly Thr Leu Ser Leu Ser Gln Arg Gln Leu
 80 85 90

Ser Glu Glu Glu Arg Gly Arg Leu Arg Asp Val Ala Ala Leu Asn
 95 100 105

Gly Leu Tyr Arg Val Arg Ile Pro Arg Arg Pro Gly Ala Leu Asp
 110 115 120

Gly Leu Glu Ala Gly Gly Tyr Val Ser Ser Phe Val Pro Ala Cys
 125 130 135

Ser Leu Val Glu Ser His Leu Ser Asp Gln Leu Thr Leu His Val
 140 145 150

Asp Val Ala Gly Asn Val Val Gly Val Ser Val Val Thr His Pro
 155 160 165

Gly Gly Cys Arg Gly His Glu Val Glu Asp Val Asp Leu Glu Leu
 170 175 180

Phe Asn Thr Ser Val Gln Leu Gln Pro Pro Thr Thr Ala Pro Gly
 185 190 195

Pro Glu Thr Ala Ala Phe Ile Glu Arg Leu Glu Met Glu Gln Ala
 200 205 210

Gln Lys Ala Lys Asn Pro Gln Glu Gln Lys Ser Phe Phe Ala Lys
 215 220 225

Tyr Trp Met Tyr Ile Ile Pro Val Val Leu Phe Leu Met Met Ser
 230 235 240

Gly Ala Pro Asp Thr Gly Gly Gln Gly Gly Gly Gly Gly Gly Gly
 245 250 255

Gly Gly Gly Ser Gly Leu Cys Cys Val Pro Pro Ser Leu
 260 265

<210> 373
 <211> 1706
 <212> DNA
 <213> Homo sapiens

<400> 373
 ggagcgctgc tggaacccga gccggagccg gagccacagc ggggagggtg 50
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 cagcaggtcg tccggggggcc caccatgctg gtgactgcct accttgcttt 150
 tgtaggcctc ctggcctcct gcctggggct ggaactgtca agatgccggg 200

ctaaacccccc tggaaaggccc tgcagcaatc ctccttcct tcggtttcaa 250
ctggacttct atcaggctcta ctccctggcc ctggcagctg attggcttca 300
ggccccctac ctctataaac tctaccagca ttactacttc ctggaaggc 350
aaattgccat cctctatgtc tgtggccttg cctctacagt cctcttggc 400
ctagtggcct ctccttgcgt ggattggctg ggtcgcaaga attcttgtgt 450
cctcttctcc ctgacttact cactatgtc cttaacccaa ctctctcaag 500
actactttgt gctgcttagtg gggcgagcac ttggtggtt gtccacagcc 550
ctgctcttct cagcccttcga ggcctggtat atccatgagc acgtggaacg 600
qcatgacttc cctgctgagt ggatcccagc tacctttgtc cgagctgcct 650
tctggaacca tgtgctggct gtagtggcag gtgtggcagc tgaggctgta 700
gccagctgga tagggctggg gcctgttagcg ccctttgtgg ctgccatccc 750
tctcctggct ctggcagggg ccttggccct tcgaaactgg ggggagaact 800
atgaccggca gcgtgccttc tcaaggacct gtgctggagg cctgcgctgc 850
ctcctgtcgg accgcccgcgt gctgctgtc ggcaccatac aagctctatt 900
tgagagtgtc atttcatct ttgtcttcct ctggacacct gtgctggacc 950
cacacggggc ccctctgggc attatcttct ccagttcat ggcagccagc 1000
ctgcttggct ctccctgtc ccgtatcgcc acctccaaga ggtaccacct 1050
tcagccccatg caccgtctgt ccctgtctgt gctcatcgtc gtcttcttc 1100
tcttcatgtt gactttctct accagccag gccaggagag tccggtgag 1150
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tcttcaccgt ggttaaggcat gatgctgagc tgcgggtacc ttcacccat 1450
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gggacagact cttgaattcc agctatccgg gattgtacag atctctctgt 1550
gactgacttt gtgactgtcc tgtggtttct cctgccatttgc ctgtgtttt 1600
gggaggacat gatgggggtt atggactgga aagaagggtgc caaaaagttcc 1650

ctctgtgtta ctcccatatc gaaaataaac actttaaat gatcaaaaaa 1700

aaaaaa 1706

<210> 374

<211> 450

<212> PRT

<213> Homo sapiens

<400> 374

Met Leu Val Thr Ala Tyr Leu Ala Phe Val Gly Leu Leu Ala Ser
1 5 10 15

Cys Leu Gly Leu Glu Leu Ser Arg Cys Arg Ala Lys Pro Pro Gly
20 25 30

Arg Ala Cys Ser Asn Pro Ser Phe Leu Arg Phe Gln Leu Asp Phe
35 40 45

Tyr Gln Val Tyr Phe Leu Ala Leu Ala Asp Trp Leu Gln Ala
50 55 60

Pro Tyr Leu Tyr Lys Leu Tyr Gln His Tyr Tyr Phe Leu Glu Gly
65 70 75

Gln Ile Ala Ile Leu Tyr Val Cys Gly Leu Ala Ser Thr Val Leu
80 85 90

Phe Gly Leu Val Ala Ser Ser Leu Val Asp Trp Leu Gly Arg Lys
95 100 105

Asn Ser Cys Val Leu Phe Ser Leu Thr Tyr Ser Leu Cys Cys Leu
110 115 120

Thr Lys Leu Ser Gln Asp Tyr Phe Val Leu Leu Val Gly Arg Ala
125 130 135

Leu Gly Gly Leu Ser Thr Ala Leu Leu Phe Ser Ala Phe Glu Ala
140 145 150

Trp Tyr Ile His Glu His Val Glu Arg His Asp Phe Pro Ala Glu
155 160 " 165

Trp Ile Pro Ala Thr Phe Ala Arg Ala Ala Phe Trp Asn His Val
170 175 180

Leu Ala Val Val Ala Gly Val Ala Ala Glu Ala Val Ala Ser Trp
185 190 195

Ile Gly Leu Gly Pro Val Ala Pro Phe Val Ala Ala Ile Pro Leu
200 205 210

Leu Ala Leu Ala Gly Ala Leu Ala Leu Arg Asn Trp Gly Glu Asn
215 220 225

Tyr Asp Arg Gln Arg Ala Phe Ser Arg Thr Cys Ala Gly Gly Leu
230 235 240

Arg Cys Leu Leu Ser Asp Arg Arg Val Leu Leu Leu Gly Thr Ile
 245 250 255
 Gln Ala Leu Phe Glu Ser Val Ile Phe Ile Phe Val Phe Leu Trp
 260 265 270
 Thr Pro Val Leu Asp Pro His Gly Ala Pro Leu Gly Ile Ile Phe
 275 280 285
 Ser Ser Phe Met Ala Ala Ser Leu Leu Gly Ser Ser Leu Tyr Arg
 290 295 300
 Ile Ala Thr Ser Lys Arg Tyr His Leu Gln Pro Met His Leu Leu
 305 310 315
 Ser Leu Ala Val Leu Ile Val Val Phe Ser Leu Phe Met Leu Thr
 320 325 330
 Phe Ser Thr Ser Pro Gly Gln Glu Ser Pro Val Glu Ser Phe Ile
 335 340 345
 Ala Phe Leu Leu Ile Glu Leu Ala Cys Gly Leu Tyr Phe Pro Ser
 350 355 360
 Met Ser Phe Leu Arg Arg Lys Val Ile Pro Glu Thr Glu Gln Ala
 365 370 375
 Gly Val Leu Asn Trp Phe Arg Val Pro Leu His Ser Leu Ala Cys
 380 385 390
 Leu Gly Leu Leu Val Leu His Asp Ser Asp Arg Lys Thr Gly Thr
 395 400 405
 Arg Asn Met Phe Ser Ile Cys Ser Ala Val Met Val Met Ala Leu
 410 415 420
 Leu Ala Val Val Gly Leu Phe Thr Val Val Arg His Asp Ala Glu
 425 430 435
 Leu Arg Val Pro Ser Pro Thr Glu Glu Pro Tyr Ala Pro Glu Leu
 440 445 450

<210> 375
 <211> 1098
 <212> DNA
 <213> Artificial

<400> 375
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 gccctggaga tggtccccgg cggcgccggc tggtgttgtc tcgtgctctg 100
 gctccccggc tgcgtcgccgg cccacggctt ccgtatccat gattatttgt 150
 actttcaagt gctgagtcct ggggacattc gatacatctt cacagccaca 200
 cctgccaagg actttggtgg tatcttcac acaaggtatg agcagattca 250

ccttgcctcc gctgaacctc cagaggcctg cggggaaactc agcaacggtt 300
 tcttcatcca ggaccagatt gctctggtgg agaggggggg ctgctccttc 350
 ctctccaaga ctcggttgtt ccaggagcac ggcgggcggg cggtgatcat 400
 ctctgacaac gcagttgaca atgacagctt ctacgtggag atgatccagg 450
 acagtaccca ggcacagct gacatccccg ccctcttcct gctcgccga 500
 gacggctaca tgatccgccc ctctctgaa cagcatgggc tgccatggc 550
 catcatttcc atcccaagtca atgtcaccag catccccacc tttgagctgc 600
 tgcaaccgcc ctggaccttc tggtagaaga gtttgccca cattccagcc 650
 ataagtgact ctgagctggg aaggggaaac ccaggaattt tgctacttgg 700
 aatttggaga tagcatctgg ggacaagtgg agccaggtag aggaaaagg 750
 tttggcggtt gctaggctga aagggaaagcc acaccactgg cttcccttc 800
 cccagggccc ccaagggtgt ctcatgtac aagaagagcc aagagacagg 850
 ccccagggtct tctggctaga acccgaaaca aaaggagctg aaggcaggtg 900
 gcctgagagc catctgtgac ctgtcacact cacctggctc cagcctcccc 950
 tacccaggggt ctctgcacag tgaccttcac agcagttgtt ggagtggttt 1000
 aaagagctgg tgtttggga ctcaataaac cctcaactgac ttttagcaa 1050
 taaagcttct catcagggtt gcaaaaaaaaaaaaaaaa 1098

<210> 376

<211> 188

<212> PRT

<213> Homo sapiens

<400> 376

Met	Val	Pro	Gly	Ala	Ala	Gly	Trp	Cys	Cys	Leu	Val	Leu	Trp	Leu
1				5				10	"				15	

Pro	Ala	Cys	Val	Ala	Ala	His	Gly	Phe	Arg	Ile	His	Asp	Tyr	Leu
				20				25					30	

Tyr	Phe	Gln	Val	Leu	Ser	Pro	Gly	Asp	Ile	Arg	Tyr	Ile	Phe	Thr
				35				40					45	

Ala	Thr	Pro	Ala	Lys	Asp	Phe	Gly	Gly	Ile	Phe	His	Thr	Arg	Tyr
				50				55					60	

Glu	Gln	Ile	His	Leu	Val	Pro	Ala	Glu	Pro	Pro	Glu	Ala	Cys	Gly
				65				70					75	

Glu	Leu	Ser	Asn	Gly	Phe	Phe	Ile	Gln	Asp	Gln	Ile	Ala	Leu	Val
				80				85					90	

Glu Arg Gly Gly Cys Ser Phe Leu Ser Lys Thr Arg Val Val Gln
 95 100 105
 Glu His Gly Gly Arg Ala Val Ile Ile Ser Asp Asn Ala Val Asp
 110 115 120
 Asn Asp Ser Phe Tyr Val Glu Met Ile Gln Asp Ser Thr Gln Arg
 125 130 135
 Thr Ala Asp Ile Pro Ala Leu Phe Leu Leu Gly Arg Asp Gly Tyr
 140 145 150
 Met Ile Arg Arg Ser Leu Glu Gln His Gly Leu Pro Trp Ala Ile
 155 160 165
 Ile Ser Ile Pro Val Asn Val Thr Ser Ile Pro Thr Phe Glu Leu
 170 175 180
 Leu Gln Pro Pro Trp Thr Phe Trp
 185

 <210> 377
 <211> 496
 <212> DNA
 <213> Artificial

 <220>
 <221> unsure
 <222> 396
 <223> unknown base

 <400> 377
 tctgcctcca ctgctctgtg ctggatcat ggaacttgca ctgctgtgtg 50
 ggctgggtt gatggcttgt gtgattccaa tccagggcgg gatcctgaac 100
 ctgaacaaga tggtaagca agtgactggg aaaatgccc tcccttccta 150
 ctggccctac ggctgtcact gcggactagg tggcagaggc caacccaaag 200
 atgccacgga ctggtgctgc cagacccatg actgctgcta tgaccacctg 250
 aagacccagg ggtgcggcat ctacaaggac aacaacaaaa gcagcataca 300
 ttgtatggat ttatctcaac gctattgtt aatggctgtg ttaatgtga 350
 tctatctgga aaatgaggac tccgaataaa aagctattac tawtnaaaa 400
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 496

 <210> 378
 <211> 116
 <212> PRT
 <213> Homo sapiens

 <400> 378

Met Glu Leu Ala Leu Leu Cys Gly Leu Val Val Met Ala Gly Val
1 5 10 15

Ile Pro Ile Gln Gly Gly Ile Leu Asn Leu Asn Lys Met Val Lys
20 25 30

Gln Val Thr Gly Lys Met Pro Ile Leu Ser Tyr Trp Pro Tyr Gly
35 40 45

Cys His Cys Gly Leu Gly Gly Arg Gly Gln Pro Lys Asp Ala Thr
50 55 60

Asp Trp Cys Cys Gln Thr His Asp Cys Cys Tyr Asp His Leu Lys
65 70 75

Thr Gln Gly Cys Gly Ile Tyr Lys Asp Asn Asn Lys Ser Ser Ile
80 85 90

His Cys Met Asp Leu Ser Gln Arg Tyr Cys Leu Met Ala Val Phe
95 100 105

Asn Val Ile Tyr Leu Glu Asn Glu Asp Ser Glu
110 115

<210> 379
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 379
ctgcctccac tgctctgtgc tggg 24

<210> 380
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 380
cagagcagtg gatgttcccc tggg 24

<210> 381
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45

<223> Synthetic construct.

<400> 381

ctgaacaaga tggtaaagca agtgactggg aaaatgccc tcctc 45

<210> 382

<211> 764

<212> DNA

<213> Homo sapiens

<400> 382

ctcgcttctt ccttctggat gggggcccaag gggggcccaagg agagtataaa 50

ggcgatgtgg agggtgccccg gcacaaccagg acgcccagtc acaggcgaga 100

gccctggat gcacccggcca gaggccatgc tgctgctgct cacgcttgcc 150

ctcctgggg gcccccacctg ggcaggaaag atgtatggcc ctggaggagg 200

caagtatttc agcaccactg aagactacga ccatgaaaatc acagggctgc 250

gggtgtctgt aggtcttctc ctggtgaaaa gtgtccaggt gaaacttgga 300

gactcctggg acgtgaaact gggagccta ggtggaaata cccaggaagt 350

caccctgcag ccaggcgaat acatcacaaa agtcttgcgc gccttccaag 400

ctttcctccg ggttatggtc atgtacacca gcaaggacccg ctatttctat 450

tttgggaagc ttgatggcca gatctcctct gcctacccca gccaagaggg 500

gcagggctg gtggccatct atggccagta tcaactcctt ggcataaga 550

gcattggctt tgaatggaat tatccactag aggagccgac cactgagcc 600

ccagtttaatc tcacataactc agcaaactca cccgtgggtc gctagggtgg 650

ggtatgggc catccgagct gaggccatct gtgtgggtgt ggctgatggt 700

actggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa 750

gcttctgcag aaaa 764

<210> 383

<211> 178

<212> PRT

<213> Homo sapiens

<400> 383

Met His Arg Pro Glu Ala Met Leu Leu Leu Leu Thr Leu Ala Leu
1 5 10 15

Leu Gly Gly Pro Thr Trp Ala Gly Lys Met Tyr Gly Pro Gly Gly
20 25 30

Gly Lys Tyr Phe Ser Thr Thr Glu Asp Tyr Asp His Glu Ile Thr
35 40 45

Gly	Leu	Arg	Val	Ser	Val	Gly	Leu	Leu	Leu	Val	Lys	Ser	Val	Gln
			50						55					60
Val	Lys	Leu	Gly	Asp	Ser	Trp	Asp	Val	Lys	Leu	Gly	Ala	Leu	Gly
			65					70					75	
Gly	Asn	Thr	Gln	Glu	Val	Thr	Leu	Gln	Pro	Gly	Glu	Tyr	Ile	Thr
			80					85					90	
Lys	Val	Phe	Val	Ala	Phe	Gln	Ala	Phe	Leu	Arg	Gly	Met	Val	Met
			95					100					105	
Tyr	Thr	Ser	Lys	Asp	Arg	Tyr	Phe	Tyr	Phe	Gly	Lys	Leu	Asp	Gly
			110				115						120	
Gln	Ile	Ser	Ser	Ala	Tyr	Pro	Ser	Gln	Glu	Gly	Gln	Val	Leu	Val
			125					130					135	
Gly	Ile	Tyr	Gly	Gln	Tyr	Gln	Leu	Leu	Gly	Ile	Lys	Ser	Ile	Gly
			140				145						150	
Phe	Glu	Trp	Asn	Tyr	Pro	Leu	Glu	Glu	Pro	Thr	Thr	Glu	Pro	Pro
			155				160						165	
Val	Asn	Leu	Thr	Tyr	Ser	Ala	Asn	Ser	Pro	Val	Gly	Arg		
			170					175						

<210> 384

<211> 2379

<212> DNA

<213> Homo sapiens

<400> 384

gctgagcgtg tgcgcggtag ggggctctcc tgccttctgg gctccaacgc 50

agctctgtgg ctgaactggg tgctcatcac ggaaactgct gggctatgga 100

atacagatgt ggcagctcag gtagccccaa attgcctgga agaatacatc 150

atgttttcg ataagaagaa attgttaggat ccagttttt ttttaaccgc 200

ccccctccca ccccccaaaa aaactgtaaa gatgcaaaaa cgtaatatcc 250

atgaagatcc tattacctag gaagatttg atgtttgct gcgaatgcgg 300

tgttgggatt tatttgttct tggagtgttc tgcgtggctg gcaaagaata 350

atgttccaaa atcggtccat ctcccaaggg gtccaaattt tcttcctgg 400

tgtcagcgag ccctgactca ctacagtgc gctgacaggg gctgtcatgc 450

aactggcccc taagccaaag caaaagacct aaggacgacc tttgaacaat 500

acaaaggatg ggttcaatg taatttaggt actgagcggg tcagctgtag 550

cactggttat agccccact gtcttactga caatgcttc ttctgccgaa 600

cgaggatgcc ctaaggcgtg taggtgtgaa ggcaaaatgg tatattgtga 650

atctcagaaa ttacaggaga taccctcaag tatactgct ggttgcttag 700
gtttgtccct tcgctataac agccttcaaa aacttaagta taatcaattt 750
aaagggctca accagctcac ctggctatac cttgaccata accatatcag 800
caatattgac gaaaatgctt ttaatggaat acgcagactc aaagagctga 850
ttcttagttc caatagaatc tcctatttc ttaacaatac cttcagacct 900
gtgacaaatt tacggaactt ggatctgtcc tataatcagc tgcatctct 950
gggatctgaa cagttcggg gcttgcgaa gctgctgagt ttacatttac 1000
ggtctaactc cctgagaacc atccctgtgc gaatattcca agactgccgc 1050
aacctggaac ttttggacct gggatataac cgatccgaa gtttagccag 1100
gaatgtctt gctggcatga tcagactcaa agaacttcac ctggagcaca 1150
atcaattttc caagctcaac ctggcccttt ttccaagggtt ggtcagcctt 1200
cagaaccctt acttgcatgt gaataaaatc agtgtcatag gacagaccat 1250
gtcctggacc tggagctcct tacaaaggct tgatttatca ggcaatgaga 1300
tcgaagcttt cagtgacccc agtgtttcc agtggtccc gaatctgcag 1350
cgccctcaacc tggattccaa caagctcaca tttattggtc aagagatttt 1400
ggattcttgg atatccctca atgacatcag tcttgctggg aatatatggg 1450
aatgcagcag aaatatttgc tcccttgtaa actggctgaa aagttttaaa 1500
ggtctaaggg agaatacaat tatctgtgcc agtcccaaag agctgcaagg 1550
agtaaatgtg atcgatgcag tgaagaacta cagcatctgt ggcaaaagta 1600
ctacagagag gtttgatctg gccagggtc tcccaaagcc gacgtttaag 1650
cccaagctcc ccaggccgaa gcatgagagc aaacccccctt tgcccccgac 1700
ggtgggagcc acagagcccg gcccagagac cgatgctgac gccgagcaca 1750
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ctcgcatcc tgctggttat ctacgtgtca tggaagcggt accctgcgag 1850
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gattataaac ccaccaacac ggagaccagc gagatgctgc tgaatggac 2000
gggaccctgc acctataaca aatcgggctc cagggagtgt gaggtatgaa 2050
ccattgtgat aaaaagagct cttaaaagct gggaaataag tggtgcttta 2100

ttgaactctg gtgactatca agggAACGCG atGCCCCCTTCCC 2150
tctccctctc actttgggtgg caagatcctt ccttgtccgt ttttagtgcat 2200
tcataatact ggtcattttc ctctcataaca taatcaaccc attgaaattt 2250
aaataccaca atcaatgtga agcttgaact ccggTTtaat ataataccta 2300
ttgtataaga ccctttactg attccattaa tgtcgcatTT gtttaagat 2350
aaaacttctt tcataaggtaa aaaaaaaaa 2379

<210> 385

<211> 513

<212> PRT

<213> Homo sapiens

<400> 385

Met Gly Phe Asn Val Ile Arg Leu Leu Ser Gly Ser Ala Val Ala
1 5 10 15

Leu Val Ile Ala Pro Thr Val Leu Leu Thr Met Leu Ser Ser Ala
20 25 30

Glu Arg Gly Cys Pro Lys Gly Cys Arg Cys Glu Gly Lys Met Val
35 40 45

Tyr Cys Glu Ser Gln Lys Leu Gln Glu Ile Pro Ser Ser Ile Ser
50 55 60

Ala Gly Cys Leu Gly Leu Ser Leu Arg Tyr Asn Ser Leu Gln Lys
65 70 75

Leu Lys Tyr Asn Gln Phe Lys Gly Leu Asn Gln Leu Thr Trp Leu
80 85 90

Tyr, Leu Asp His Asn His Ile Ser Asn Ile Asp Glu Asn Ala Phe
95 100 105

Asn Gly Ile Arg Arg Leu Lys Glu Leu Ile Leu Ser Ser Asn Arg
110 115 120

Ile Ser Tyr Phe Leu Asn Asn Thr Phe Arg Pro Val Thr Asn Leu
125 130 135

Arg Asn Leu Asp Leu Ser Tyr Asn Gln Leu His Ser Leu Gly Ser
140 145 150

Glu Gln Phe Arg Gly Leu Arg Lys Leu Leu Ser Leu His Leu Arg
155 160 165

Ser Asn Ser Leu Arg Thr Ile Pro Val Arg Ile Phe Gln Asp Cys
170 175 180

Arg Asn Leu Glu Leu Leu Asp Leu Gly Tyr Asn Arg Ile Arg Ser
185 190 195

Leu Ala Arg Asn Val Phe Ala Gly Met Ile Arg Leu Lys Glu Leu

200	205	210
His		
Leu	Glu	
His	Asn	Gln
Phe	Ser	Lys
215		Leu
	Asn	Leu
	Ala	Leu
	Phe	
220		225
Pro	Arg	Leu
Val	Ser	Leu
Gln	Asn	Leu
Tyr		
230		235
	Leu	Gln
	Trp	Asn
		Lys
240		
Ile	Ser	Val
Ile	Gly	Gln
Thr	Met	Ser
Trp		Trp
245		250
	Thr	Trp
	Ser	Ser
		Leu
255		
Gln	Arg	Leu
Asp	Leu	Ser
Gly		
Asn	Glu	Ile
		Glu
260		265
		Ala
	Phe	Ser
		Gly
270		
Pro	Ser	Val
Phe	Gln	Cys
Val	Pro	Asn
Leu	Gln	Arg
		Leu
		Asn
275		280
		285
Asp	Ser	Asn
Lys	Leu	Thr
Phe	Ile	Gly
Gln		
	Glu	Ile
290		295
		Leu
	Asp	Ser
		300
Trp	Ile	Ser
Leu	Asn	Asp
Ile	Ser	Leu
Ala		
Gly		
Asn	Ile	Cys
	Ser	Leu
	Val	
	Asn	Trp
305		310
		Trp
		Glu
		315
Cys	Ser	Arg
Asn	Ile	Cys
	Ser	Leu
	Val	
	Asn	Trp
320		325
		Leu
		lys
		Ser
		Phe
330		
Lys	Gly	Leu
Arg	Glu	Asn
		Thr
		Ile
		Ile
335		340
		Cys
		Ala
		Ser
		Pro
		Lys
		Glu
345		
Leu	Gln	Gly
Val	Asn	Val
Ile	Asp	Ala
		Val
		Lys
350		355
		Asn
		Tyr
		Ser
360		
Cys	Gly	Lys
Ser	Thr	Thr
	Glu	Arg
		Phe
365		370
		Asp
		Leu
		Ala
		Arg
		Ala
375		
Pro	Lys	Pro
Thr	Phe	Lys
380		385
		Pro
		Arg
		Pro
		Lys
		His
		Glu
390		
Ser	Lys	Pro
Pro	Leu	Pro
395		400
		Gly
		Ala
		Thr
		Glu
		Pro
		Gly
405		
Pro	Glu	Thr
Asp	Ala	Asp
410		415
		Ala
		Glu
		His
		Ile
		Ser
		Phe
		His
		Lys
420		
Ile	Ala	Gly
Ser	Val	Ala
425		430
		Leu
		Phe
		Leu
		Ser
		Val
		Leu
		Val
435		
Leu	Val	Ile
Tyr	Val	Ser
440		445
		Trp
		Lys
		Arg
		Tyr
		Pro
		Ala
		Ser
		Met
450		
Gln	Leu	Gln
Gln	Arg	Ser
455		460
		Leu
		Met
		Arg
		Arg
		His
		Arg
		Lys
		Lys
465		
Arg	Gln	Ser
Leu	Lys	Gln
470		475
		Met
		Thr
		Pro
		Ser
		Thr
		Gln
		Glu
		Phe
480		
Val	Asp	Tyr
Lys	Pro	Thr
485		490
		Asn
		Thr
		Glu
		Thr
		Ser
		Glu
		Met
		Leu
495		

Asn Gly Thr Gly Pro Cys Thr Tyr Asn Lys Ser Gly Ser Arg Glu
500 505 510

Cys Glu Val

<210> 386

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 386

ctgggatctg aacagttcg gggc 24

<210> 387

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 387

ggtccccagg acatggtctg tccc 24

<210> 388

<211> 48

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-48

<223> Synthetic construct.

<400> 388

gctgagttta catttacggt ctaactccct gagaaccatc cctgtgcg 48

<210> 389

<211> 1449

<212> DNA

<213> Homo sapiens

<400> 389

agttctgaga aagaaggaaa taaacacagg caccaaacca ctatcctaag 50

ttgactgtcc tttaaatatg tcaagatcca gactttcag tgtcacctca 100

gcgatctcaa cgatagggat cttgtgttg ccgcattcc agttggtgct 150

ctcggaccta ccatgcgaag aagatgaaat gtgtgtaaat tataatgacc 200

aacaccctaa tggctggat atctggatcc tcctgctgct ggtttggtg 250
gcagctcttc tctgtggagc tgtggtcctc tgcctccagt gctggctgag 300
gagaccccga attgattctc acaggcgcac catggcagtt tttgctgtg 350
gagacttgga ctctatattat gggacagaag cagctgtgag tccaactgtt 400
ggaattcacc ttcaaactca aaccctgac ctatatcctg ttcctgctcc 450
atgtttggc cctttaggct cccccacctcc atatgaagaa attgtaaaaa 500
caacctgatt ttaggtgtgg attatcaatt taaagtatta acgacatctg 550
taattccaaa acatcaaatt taggaatagt tatttcagtt gttggaaatg 600
tccagagatc tattcatata gtctgaggaa ggacaattcg acaaaagaat 650
ggatgttggaa aaaaattttg gtcatggaga tgtttaaata gtaaaagtagc 700
aggctttga tgtgtcactg ctgtatcata cttttatgct acacaaccaa 750
attaatgctt ctccactagt atccaaacag gcaacaatta ggtgctggaa 800
gtagtttcca tcacatttag gactccactg cagtatacag cacaccattt 850
tctgcttaa actctttcct agcatggggt ccataaaaat tattataatt 900
taacaatagc ccaagccgag aatccaaacat gtccagaacc agaaccagaa 950
agatagtatt tgaatgaagg tgaggggaga gagtaggaaa aagaaaagtt 1000
tggagttgaa gggtaaagga taaatgaaga gggaaaggaa aagattacaa 1050
gtctcagcaa aaacaagagg ttttatgccca caacctgaag aggaagaaat 1100
tgtagataga aggtgaagga gattgctgaa gatatacagc acatataatg 1150
ccaacacggg gagaaaagaa aatttccct tttacagtaa tgaatgtggc 1200
ctccatagtc catagtgtt ctctggagcc tcaggccttgcatatttattg 1250
cagcatcatg ctaagaacct tcggcatagg tatctgttcc catgaggact 1300
gcagaagtag caatgagaca tcttcaagtg gcattttggc agtggccatc 1350
agcaggggga cagacaaaaa catccatcac agatgacata tgatcttcag 1400
ctgacaaatt tggtaacaa aacaataaac atcaatagat atctaaaaa 1449

<210> 390

<211> 146

<212> PRT

<213> Homo sapiens

<400> 390

Met	Ser	Arg	Ser	Arg	Leu	Phe	Ser	Val	Thr	Ser	Ala	Ile	Ser	Thr
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Ile	Gly	Ile	Leu	Cys	Leu	Pro	Leu	Phe	Gln	Leu	Val	Leu	Ser	Asp	
20									25					30	
Leu	Pro	Cys	Glu	Glu	Asp	Glu	Met	Cys	Val	Asn	Tyr	Asn	Asp	Gln	
			35						40					45	
His	Pro	Asn	Gly	Trp	Tyr	Ile	Trp	Ile	Leu	Leu	Leu	Leu	Val	Leu	
				50					55					60	
Val	Ala	Ala	Leu	Leu	Cys	Gly	Ala	Val	Val	Leu	Cys	Leu	Gln	Cys	
				65					70					75	
Trp	Leu	Arg	Arg	Pro	Arg	Ile	Asp	Ser	His	Arg	Arg	Thr	Met	Ala	
				80					85					90	
Val	Phe	Ala	Val	Gly	Asp	Leu	Asp	Ser	Ile	Tyr	Gly	Thr	Glu	Ala	
				95					100					105	
Ala	Val	Ser	Pro	Thr	Val	Gly	Ile	His	Leu	Gln	Thr	Gln	Thr	Pro	
				110					115					120	
Asp	Leu	Tyr	Pro	Val	Pro	Ala	Pro	Cys	Phe	Gly	Pro	Leu	Gly	Ser	
				125					130					135	
Pro	Pro	Pro	Tyr	Glu	Glu	Ile	Val	Lys	Thr	Thr					
				140					145						
<210> 391															
<211> 26															
<212> DNA															
<213> Artificial															
<220>															
<221> Artificial Sequence															
<222> 1-26															
<223> Synthetic construct.															
<400> 391															
ctttcagtg tcacccatgc gatctc 26															
<210> 392															
<211> 23															
<212> DNA															
<213> Artificial															
<220>															
<221> Artificial Sequence															
<222> 1-23															
<223> Synthetic construct.															
<400> 392															
ccaaaacatg gagcaggaac agg 23															
<210> 393															
<211> 47															
<212> DNA															
<213> Artificial															

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 393
 ccagttggtg ctctcgacc taccatgcga agaagatgaa atgtgtg 47

<210> 394
<211> 2340
<212> DNA
<213> Homo sapiens

<400> 394
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 acccaccggc gtttctccag ctcgatctgg aggctgcttc gccagtgtgg 100
 gacgcagctg acgcccgtt attagctctc gctgcgtcgc cccggctcag 150
 aagctccgtg gcggcggcga ccgtgacgag aagcccacgg ccagctca 200
 tctcttctac tttgggagag agagaaagtc agatgcccct tttaaactcc 250
 ctcttcaaaa ctcatctcct gggtgactga gttaatagag tggataaca 300
 cttgctgaag atgaagaata tacaatattt aggatatttt tttcttttt 350
 ttttcaagtc ttgatttgc gcttacctca agttaccatt tttcagtcaa 400
 gtctgttgtt ttgcttcttc agaaatgttt tttacaatct caagaaaaaa 450
 tatgtcccgaa atttgagtt tactgttgct tgtatttgaa ctcatttggg 500
 gattgatgtt actgcactat acttttcaac aaccaagaca tcaaaggc 550
 gtcaagttac gtgagcaaat actagactta agcaaaagat atgttaaagc 600
 tctagcagag gaaaataaga acacagtgaa tgctcgaaac ggtgcttcta 650
 tggcaggata tgccgatctg aaaagaacaa ttgctgtcct tctggatgac 700
 attttgcac gattggtaa gctggagaac aaagttgact atattgttgt 750
 gaatggctca gcagccaaca ccaccaatgg tactagtggg aatttggc 800
 cagtaaccac aaataaaaga acgaatgtct cggcagttt cagatagcag 850
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 agaaaagctt tataatttgct ggcttaggac agagcaatac tttacaataa 950
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 tgtacataaa aattttaaag ttattttttt gctttcaggc aagtctgttc 1050
 aatgctgtac tatgtcctta aagagaattt ggtaacttgg ttgatgtggt 1100

aagcagatag gtgagtttg tataaatctt ttgtgttga gatcaagctg 1150
aaatgaaaac actgaaaaac atggattcat ttctataaca catttattta 1200
agtatataac acgtttttg gacaagtcaa gaatgtttaa tcattctgc 1250
atttgttctc aatagatgta actgttagac tacggctatt tgaaaaaatg 1300
tgcttattgt actatatttt gttattccaa ttatgagcag agaaaggaaa 1350
tataatgttggaaaataatgt tttgaaatca tgacccaaag aatgtattga 1400
tttgcactat cttcagaat aactgaaggt taattattgt atattttaa 1450
aaattacact tataagagta taatcttggaa atggtagca gccactgtcc 1500
attacctatc gtaaacatttggcaattta ataacagcat taaaatagg 1550
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tactttgtg ctgcattaaa ttgcttgaa agtgttaaca ttatattata 1850
taagagtatc ctttatgaaa ttttgaattt gtataacaga tgcatttagat 1900
attcatttta tataatggcc acttaaaata agaacatttta aaatataaacc 1950
tatgaagattt gactatctt tcaggaaaaaa agctgtatat agcacaggga 2000
accctaattct tggtaatttgc tagtataaaa caaatttatac ttttattttaa 2050
atttcccttg tagcaaatctt aattgccaca tgggcccta tatttcata 2100
tatttattttctt ctatagtaac tgcttaagtgc cagctagctt ctagatttag 2150
actatataaga atttagatat tgtattgttc gtcattataa tatgtaccca 2200
catgtacaa taattacaat attttattaa aataaatatg tgaaatatttgc 2250
tttcatgaaa gacagatttc caaatctctc ttctcttctc tgtactgtct 2300
acctttatgtt gaagaaatattatatttgc attgccaggt 2340

<210> 395
<211> 140
<212> PRT
<213> Homo sapiens

<400> 395
Met Phe Phe Thr Ile Ser Arg Lys Asn Met Ser Gln Lys Leu Ser
1 5 10 15

Leu	Leu	Leu	Leu	Val	Phe	Gly	Leu	Ile	Trp	Gly	Leu	Met	Leu	Leu
				20					25				30	
His	Tyr	Thr	Phe	Gln	Gln	Pro	Arg	His	Gln	Ser	Ser	Val	Lys	Leu
				35					40				45	
Arg	Glu	Gln	Ile	Leu	Asp	Leu	Ser	Lys	Arg	Tyr	Val	Lys	Ala	Leu
				50					55				60	
Ala	Glu	Glu	Asn	Lys	Asn	Thr	Val	Asp	Val	Glu	Asn	Gly	Ala	Ser
				65					70				75	
Met	Ala	Gly	Tyr	Ala	Asp	Leu	Lys	Arg	Thr	Ile	Ala	Val	Leu	Leu
				80					85				90	
Asp	Asp	Ile	Leu	Gln	Arg	Leu	Val	Lys	Leu	Glu	Asn	Lys	Val	Asp
				95					100				105	
Tyr	Ile	Val	Val	Asn	Gly	Ser	Ala	Ala	Asn	Thr	Thr	Asn	Gly	Thr
				110					115				120	
Ser	Gly	Asn	Leu	Val	Pro	Val	Thr	Thr	Asn	Lys	Arg	Thr	Asn	Val
				125					130				135	
Ser	Gly	Ser	Ile	Arg										
				140										

<210> 396

<211> 2639

<212> DNA

<213> Homo sapiens

<400> 396

cgcggccggg ccgccgggt gagcgtgccg aggccgctgt ggcgcaggct 50

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gggcccagac aaccggcca tgcttccccg ggtgccaatg cgaggtggag 150

accttcggcc ttttcgacag cttcagcctg actcggtgg attgttagcgg 200

cctggggccc cacatcatgc cggtgcccatt ccctctggac acagcccact 250

tggacctgtc ctccaaccgg ctggagatgg tgaatgagtc ggtgttggcg 300

gggcccggct acacgacggt ggctggcctg gatctcagcc acaacctgct 350

caccagcatc tcacccactg cttctcccg cttcgctac ctggagtcgc 400

ttgacctcag ccacaatggc ctgacagccc tgccagccga gagcttcacc 450

agctcacccc tgagcgacgt gaaccttagc cacaaccaggc tccgggaggt 500

ctcagtgtct gccttcacga cgcacagtcg gggccggca ctacacgtgg 550

acctctccca caacctcatt caccgcctcg tgccccaccc cacgagggcc 600

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<210> 397

<211> 353

<212> PRT

<213> Homo sapiens

<400> 397

Met	Pro	Trp	Pro	Leu	Leu	Leu	Leu	Ala	Val	Ser	Gly	Ala	Gln	
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Thr	Thr	Arg	Pro	Cys	Phe	Pro	Gly	Cys	Gln	Cys	Glu	Val	Glu	Thr
				20				25				30		
Phe	Gly	Leu	Phe	Asp	Ser	Phe	Ser	Leu	Thr	Arg	Val	Asp	Cys	Ser
				35				40				45		
Gly	Leu	Gly	Pro	His	Ile	Met	Pro	Val	Pro	Ile	Pro	Leu	Asp	Thr
				50				55				60		
Ala	His	Leu	Asp	Leu	Ser	Ser	Asn	Arg	Leu	Glu	Met	Val	Asn	Glu
				65				70				75		
Ser	Val	Leu	Ala	Gly	Pro	Gly	Tyr	Thr	Thr	Leu	Ala	Gly	Leu	Asp
				80				85				90		
Leu	Ser	His	Asn	Leu	Leu	Thr	Ser	Ile	Ser	Pro	Thr	Ala	Phe	Ser
				95				100				105		
Arg	Leu	Arg	Tyr	Leu	Glu	Ser	Leu	Asp	Leu	Ser	His	Asn	Gly	Leu
				110				115				120		
Thr	Ala	Leu	Pro	Ala	Glu	Ser	Phe	Thr	Ser	Ser	Pro	Leu	Ser	Asp
				125				130				135		
Val	Asn	Leu	Ser	His	Asn	Gln	Leu	Arg	Glu	Val	Ser	Val	Ser	Ala
				140				145				150		

Phe Thr Thr His Ser Gln Gly Arg Ala Leu His Val Asp Leu Ser
 155 160 165
 His Asn Leu Ile His Arg Leu Val Pro His Pro Thr Arg Ala Gly
 170 175 180
 Leu Pro Ala Pro Thr Ile Gln Ser Leu Asn Leu Ala Trp Asn Arg
 185 190 195
 Leu His Ala Val Pro Asn Leu Arg Asp Leu Pro Leu Arg Tyr Leu
 200 205 210
 Ser Leu Asp Gly Asn Pro Leu Ala Val Ile Gly Pro Gly Ala Phe
 215 220 225
 Ala Gly Leu Gly Gly Leu Thr His Leu Ser Leu Ala Ser Leu Gln
 230 235 240
 Arg Leu Pro Glu Leu Ala Pro Ser Gly Phe Arg Glu Leu Pro Gly
 245 250 255
 Leu Gln Val Leu Asp Leu Ser Gly Asn Pro Lys Leu Asn Trp Ala
 260 265 270
 Gly Ala Glu Val Phe Ser Gly Leu Ser Ser Leu Gln Glu Leu Asp
 275 280 285
 Leu Ser Gly Thr Asn Leu Val Pro Leu Pro Glu Ala Leu Leu Leu
 290 295 300
 His Leu Pro Ala Leu Gln Ser Val Ser Val Gly Gln Asp Val Arg
 305 310 315
 Cys Arg Arg Leu Val Arg Glu Gly Thr Tyr Pro Arg Arg Pro Gly
 320 325 330
 Ser Ser Pro Lys Val Pro Leu His Cys Val Asp Thr Arg Glu Ser
 335 340 345
 Ala Ala Arg Gly Pro Thr Ile Leu
 350

<210> 398

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 398

ccctgcgcagc cgagagcttc acc 23

<210> 399

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 399
ggttggtgcc cgaaagggcc agc 23

<210> 400

<211> 44

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-44

<223> Synthetic construct.

<400> 400
caaccccaag cttaactggg caggagctga ggtgtttca ggcc 44

<210> 401

<211> 1571

<212> DNA

<213> Homo sapiens

<400> 401
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atgtcattct ctatctattc actgcaagtg cctgctgttc caggccttac 200
ctgctggca ctaacggcg agccaggatg gggacagaat aaaggagcca 250
cgacctgtgc caccaactcg cactcagact ctgaactcag acctgaaatc 300
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ctgcgtttta tctccttatgg actccttcca ctggactgaa gacactcaat 450
ttggaaagct gtgtgatcgc cacaacaccc cagggaaatac gaaatggatt 500
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ccaattccctt tcttaccatc aagaaggacc tccggctctc tcatgcccac 750

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gggaactaga cattcttctg caatggatgg aggagacaga ataggaggaa 900
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atttttgtaa tattttctg ctattggata tatttatttag ttaatatatt 1150
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ctaggggggt tattcatttgc tattcaacta aggacatatt tactcatgt 1350
gatgctctgt gagatatttgc aaatttgcacc aatgactact taggatgggt 1400
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ccatccccag tagactcccc agtcccataa ttgtgtatct tccagccagg 1500
aatcctacac ggccagcatg tatttctaca aataaaatgtt tctttgcata 1550
ccaaaaaaaaa aaaaaaaaaa a 1571

<210> 402

<211> 261

<212> PRT

<213> Homo sapiens

<400> 402

Met	Arg	Gln	Phe	Pro	Lys	Thr	Ser	Phe	Asp	Ile	Ser	Pro	Glu	Met
1														15

Ser	Phe	Ser	Ile	Tyr	Ser	Leu	Gln	Val	Pro	Ala	Val	Pro	Gly	Leu
														30

Thr	Cys	Trp	Ala	Leu	Thr	Ala	Glu	Pro	Gly	Trp	Gly	Gln	Asn	Lys
														45

Gly	Ala	Thr	Thr	Cys	Ala	Thr	Asn	Ser	His	Ser	Asp	Ser	Glu	Leu
														60

Arg	Pro	Glu	Ile	Phe	Ser	Ser	Arg	Glu	Ala	Trp	Gln	Phe	Phe	Leu
														75

Leu	Leu	Trp	Ser	Pro	Asp	Phe	Arg	Pro	Lys	Met	Lys	Ala	Ser	Ser
														90

<210> 403

<211> 28

<212> DNA

<213> Artificial

<220>

<221> Ar

<222> 1-28

<223> Synthetic co

<400> 403

ctcctgtgg ctccagattt caggccta 28

<210> 404

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-26

223 Synt

<400> 404
 agtccctcctt aagattctga tgtcaa 26

 <210> 405
 <211> 998
 <212> DNA
 <213> Homo sapiens

 <400> 405
 ccgttatcgt cttgcgctac tgctgaatgt ccgtcccgga ggaggaggag 50
 aggctttgc cgctgaccga gagatggccc cgagcgagca aattcctact 100
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 tcacaaaaac tcgactccaa atgcaaggag aagcagctct tgctcggttg 200
 ggagacggtg caagagaatc tgccccctat agggaatgg tgcgcacagc 250
 cctagggatc attgaagagg aaggcttct aaagcttgg caaggagtga 300
 cacccgccccat ttacagacac gtatgttatt ctggaggtcg aatggtcaca 350
 tatgaacatc tccgagaggt tgtgtttggc aaaagtgaag atgagcatta 400
 tccccttgg aaatcagtca ttggagggat gatggctggt gttattggcc 450
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 ggaaaaagga aactggaagg aaaaccattt cgatttcgtg gtgtacatca 550
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 accacttatg atacagtgaa acactacttg gtattgaata caccacttga 700
 ggacaatatc atgactcactg gtttatcaag tttatgttct ggactggtag 750
 cttctattct ggaaacacca gccgatgtca tcaaaagcag aataatgaat 800
 caaccacgag ataaacaagg aaggggactt ttgtataat catcgactga 850
 ctgcttgatt caggctgttc aaggtgaagg attcatgagt ctatataaag 900
 gcttttacc atcttggctg agaatgaccc ctttgtcaat ggtttctgg 950
 cttacttatg aaaaaatcag agagatgagt ggagtcagtc cattttaa 998

 <210> 406
 <211> 323
 <212> PRT
 <213> Homo sapiens

 <400> 406
 Met Ser Val Pro Glu Glu Glu Glu Arg Leu Leu Pro Leu Thr Gln
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Arg Trp Pro Arg Ala Ser Lys Phe Leu Leu Ser Gly Cys Ala Ala
 20 25 30

Thr Val Ala Glu Leu Ala Thr Phe Pro Leu Asp Leu Thr Lys Thr
 35 40 45

Arg Leu Gln Met Gln Gly Glu Ala Ala Leu Ala Arg Leu Gly Asp
 50 55 60

Gly Ala Arg Glu Ser Ala Pro Tyr Arg Gly Met Val Arg Thr Ala
 65 70 75

Leu Gly Ile Ile Glu Glu Gly Phe Leu Lys Leu Trp Gln Gly
 80 85 90

Val Thr Pro Ala Ile Tyr Arg His Val Val Tyr Ser Gly Gly Arg
 95 100 105

Met Val Thr Tyr Glu His Leu Arg Glu Val Val Phe Gly Lys Ser
 110 115 120

Glu Asp Glu His Tyr Pro Leu Trp Lys Ser Val Ile Gly Gly Met
 125 130 135

Met Ala Gly Val Ile Gly Gln Phe Leu Ala Asn Pro Thr Asp Leu
 140 145 150

Val Lys Val Gln Met Gln Met Glu Gly Lys Arg Lys Leu Glu Gly
 155 160 165

Lys Pro Leu Arg Phe Arg Gly Val His His Ala Phe Ala Lys Ile
 170 175 180

Leu Ala Glu Gly Gly Ile Arg Gly Leu Trp Ala Gly Trp Val Pro
 185 190 195

Asn Ile Gln Arg Ala Ala Leu Val Asn Met Gly Asp Leu Thr Thr
 200 205 210

Tyr Asp Thr Val Lys His Tyr Leu Val Leu Asn Thr Pro Leu Glu
 215 220 225

Asp Asn Ile Met Thr His Gly Leu Ser Ser Leu Cys Ser Gly Leu
 230 235 240

Val Ala Ser Ile Leu Gly Thr Pro Ala Asp Val Ile Lys Ser Arg
 245 250 255

Ile Met Asn Gln Pro Arg Asp Lys Gln Gly Arg Gly Leu Leu Tyr
 260 265 270

Lys Ser Ser Thr Asp Cys Leu Ile Gln Ala Val Gln Gly Glu Gly
 275 280 285

Phe Met Ser Leu Tyr Lys Gly Phe Leu Pro Ser Trp Leu Arg Met
 290 295 300

Thr Pro Trp Ser Met Val Phe Trp Leu Thr Tyr Glu Lys Ile Arg

305

310

315

Glu Met Ser Gly Val Ser Pro Phe
320

<210> 407

<211> 31

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-31

<223> Synthetic construct.

<400> 407

cgcgatccc gttatcgctc tgcgctactg c 31

<210> 408

<211> 34

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-34

<223> Synthetic construct.

<400> 408

gcggattct taaaatggac tgactccact catc 34

<210> 409

<211> 1487

<212> DNA

<213> Homo sapiens

<400> 409

cggacgcgtg ggcgcgggac gccggcaggg ttgtggcgca gcagtctcct 50

tcctgcgcgc gcgcctgaag tcggcgtggg cgtttgagga agctggata 100

cagcatttaa tgaaaaattt atgcttaaga agtaaaaätg gcaggcttcc 150

tagataattt tcgttggcca gaatgtaat gtattgactg gagtgagaga 200

agaaaatgctg tggcatctgt tgtcgägg atattgtttt ttacaggctg 250

gtggataatg attgatgcag ctgtggta tcctaagcca gaacagttga 300

accatgcctt tcacacatgt ggtgtatccc ccacattggc tttcttcatg 350

ataaaatgctg tatccaatgc tcaggtgaga ggtgatagct atgaaagcgg 400

ctgttttagga agaacaggtg ctcgagttt gcttttcatt ggtttcatgt 450

tgtatgtttgg gtcacttatt gcttccatgt ggattctttt tggtgcatat 500

gttacccaaa atactgatgt ttatccggga ctagctgtgt ttttcaaaa 550

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cataaaaggt tttcagcaag ttgttaactt ttttggccta aaaatgaggt 1350
ttttttggta aagaaaaat atttgttctt atgtattgaa gaagtgtact 1400
tttatataat gatttttaa atgccccaaag gactagttg aaagcttctt 1450
ttaaaaagaa ttccctctaat atgactttat gtgagaa 1487

<210> 410
<211> 158
<212> PRT
<213> Homo sapiens

<400> 410
Met Ala Gly Phe Leu Asp Asn Phe Arg Trp Pro Glu Cys Glu Cys
1 5 10 15
Ile Asp Trp Ser Glu Arg Arg Asn Ala Val Ala Ser Val Val Ala
20 25 30
Gly Ile Leu Phe Phe Thr Gly Trp Trp Ile Met Ile Asp Ala Ala
35 40 45
Val Val Tyr Pro Lys Pro Glu Gln Leu Asn His Ala Phe His Thr
50 55 60
Cys Gly Val Phe Ser Thr Leu Ala Phe Phe Met Ile Asn Ala Val
65 70 75

Ser Asn Ala Gln Val Arg Gly Asp Ser Tyr Glu Ser Gly Cys Leu
 80 85 90
 Gly Arg Thr Gly Ala Arg Val Trp Leu Phe Ile Gly Phe Met Leu
 95 100 105
 Met Phe Gly Ser Leu Ile Ala Ser Met Trp Ile Leu Phe Gly Ala
 110 115 120
 Tyr Val Thr Gln Asn Thr Asp Val Tyr Pro Gly Leu Ala Val Phe
 125 130 135
 Phe Gln Asn Ala Leu Ile Phe Phe Ser Thr Leu Ile Tyr Lys Phe
 140 145 150
 Gly Arg Thr Glu Glu Leu Trp Thr
 155

 <210> 411
 <211> 20
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

 <400> 411
 gttgaggaa gctgggatac 20

 <210> 412
 <211> 20
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

 <400> 412
 ccaaactcga gcacctgttc 20

 <210> 413
 <211> 40
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-40
 <223> Synthetic construct.

 <400> 413
 atggcaggct tcctagataa ttttcgttgg ccagaatgtg 40

 <210> 414

<211> 1337
<212> DNA
<213> Homo sapiens

<400> 414
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actgcatacta gaggagggcc gtctgtgagg ccactacccc tccagcaact 150
gggaggtgg actgtcagaa gctggccag ggtggtggtc agctgggtca 200
gggacctacg gcacctgctg gaccacctcg ccttctccat cgaagcaggg 250
aagtgggagc ctcgagccct cgggtggaag ctgaccccaa gccacccttc 300
acctggacag gatgagagtg tcaggtgtgc ttcccttcct ggccctcatc 350
tttgcctatag tcacgacatg gatgtttatt cgaagctaca tgagcttcag 400
catgaaaacc atccgtctgc cacgctggct ggcagcctcg cccaccaagg 450
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aactacttg cgtttaaat ctgcagtggg gccgccaacg tcgtgggccc 550
tactatgtgc tttaaagacc gcatgatcat gagtcctgtg aaaaacaatg 600
tgggcaaggagg cctaaacatc gccctggtga atgaaaccac gggagctgtg 650
ctgggacaga aggcatgtga catgtactct ggagatgtta tgcacctagt 700
gaaattcctt aaagaaattc cgggggggtgc actggtgctg gtggcctcct 750
acgacgatcc agggacccaa atgaacgatg aaagcagggaa actcttctct 800
gacttgggga gttcctacgc aaaacaactg ggctccggg acagctgggt 850
cttcataatggg gccaaagacc tcagggtaa aagccccctt gagcagttct 900
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tcccacagca catcctaccc ggaagaccag cctcagaggg tccttctgga 1200
accagctgtc tgtggagaga atggggtgtct ttcgtcaggg actgctgacg 1250
gctggtcctg aggaaggaca aactgcccag acttgagccc aattaaattt 1300
tatttttgtct ggtttgaaa aaaaaaaaaa aaaaaaaaa 1337

<210> 415

<211> 224

<212> PRT

<213> Homo sapiens

<400> 415

Met Arg Val Ser Gly Val Leu Arg Leu Leu Ala Leu Ile Phe Ala
1 5 10 15

Ile Val Thr Thr Trp Met Phe Ile Arg Ser Tyr Met Ser Phe Ser
20 25 30

Met Lys Thr Ile Arg Leu Pro Arg Trp Leu Ala Ala Ser Pro Thr
35 40 45

Lys Glu Ile Gln Val Lys Lys Tyr Lys Cys Gly Leu Ile Lys Pro
50 55 60

Cys Pro Ala Asn Tyr Phe Ala Phe Lys Ile Cys Ser Gly Ala Ala
65 70 75

Asn Val Val Gly Pro Thr Met Cys Phe Glu Asp Arg Met Ile Met
80 85 90

Ser Pro Val Lys Asn Asn Val Gly Arg Gly Leu Asn Ile Ala Leu
95 100 105

Val Asn Gly Thr Thr Gly Ala Val Leu Gly Gln Lys Ala Phe Asp
110 115 120

Met Tyr Ser Gly Asp Val Met His Leu Val Lys Phe Leu Lys Glu
125 130 135

Ile Pro Gly Gly Ala Leu Val Leu Val Ala Ser Tyr Asp Asp Pro
140 145 150

Gly Thr Lys Met Asn Asp Glu Ser Arg Lys Leu Phe Ser Asp Leu
155 160 165

Gly Ser Ser Tyr Ala Lys Gln Leu Gly Phe Arg Asp Ser Trp Val
170 175 180

Phe Ile Gly Ala Lys Asp Leu Arg Gly Lys Ser Pro Phe Glu Gln
185 190 195

Phe Leu Lys Asn Ser Pro Asp Thr Asn Lys Tyr Glu Gly Trp Pro
200 205 210

Glu Leu Leu Glu Met Glu Gly Cys Met Pro Pro Lys Pro Phe
215 220

<210> 416

<211> 21

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-21
<223> Synthetic construct.

<400> 416
gccatagtca cgacatggat g 21

<210> 417
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 417
ggatggccag agctgctg 18

<210> 418
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-26
<223> Synthetic construct.

<400> 418
aaagtacaag tgtggcctca tcaagc 26

<210> 419
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 419
tctgactcct aagtcaaggca ggag 24

<210> 420
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 420
attctctcca cagacagctg gttc 24

<210> 421
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 421
gtacaagtgt ggcctcatca agccctgcc agccaactac tttgcg 46

<210> 422
<211> 1701
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1528
<223> unknown base

<400> 422
gagactgcag agggagataa agagagaggg caaagaggca gcaagagatt 50
tgtcctgggg atccagaaac ccatgataacc ctactgaaca ccgaatcccc 100
tggaaagccc cagagacaga gacagcaaga gaagcagaga taaatacact 150
cacgccagga gctcgctcgc tctctctc tctctctcac tcctccctcc 200
ctctctctct gcctgtccta gcctcttagt cctcaaattc ccagtccct 250
gcacccttc ctggacact atgttgtct ccgcctcct gctggaggtg 300
atttggatcc tggctgcaga tgggggtcaa cactggacgt atgagggcc 350
acatggtcag gaccattggc cagccttta ccctgagtgt ggaaacaatg 400
cccagtcgcc catcgatatt cagacagaca gtgtgacatt tgaccctgat 450
ttgcctgctc tgcagcccca cgatatgac cagcctggca ccgagcctt 500
ggacctgcac aacaatggcc acacagtgca actctctctg ccctctaccc 550
tgtatctggg tggacttccc cgaaaatatg tagctgccc gctccacctg 600
cactggggtc agaaaggatc cccagggggg tcagaacacc agatcaacag 650
tgaagccaca tttgcagagc tccacattgt acattatgac tctgattcct 700
atgacagctt gagtgaggct gctgagaggc ctcagggcct ggctgtcctg 750
ggcatcctaa ttgaggtggg tgagactaag aatatacgat atgaacacat 800
tctgagtcac ttgcatgaag tcaggcataa agatcagaag acctcagtgc 850

ctcccttcaa cctaagagag ctgctcccc aacagctggg gcagtacttc 900
cgctacaatg gctcgctcac aactccccct tgctaccaga gtgtgctctg 950
gacagtttt tatagaaggt cccagattc aatggaacag ctggaaaagc 1000
ttcaggggac attgttctcc acagaagagg agccctctaa gcttctggta 1050
cagaactacc gagcccttca gcctctcaat cagcgcatgg tctttgcttc 1100
tttcatccaa gcaggatcct cgataccac aggtgaaatg ctgagtctag 1150
gtgttagaat cttgggttggc tgtctctgcc ttctcctggc tggtttatttc 1200
attgctagaa agattcggaa gaagaggctg gaaaaccgaa agagtgtgg 1250
cttcacctca gcacaagcca cgactgaggc ataaattcct tctcagatac 1300
catggatgtg gatgacttcc cttcatgcct atcaggaagc ctctaaaatg 1350
gggtgttagga tctggccaga aacactgttag gagtagtaag cagatgtcct 1400
ccttcccctg gacatctctt agagaggaat ggacccaggc tgtcattcca 1450
ggaagaactg cagagccttc agcctctcca aacatgttagg aggaaatgag 1500
gaaatcgctg tgggttaat gcagaganca aactctgttt agttgcaggg 1550
gaagtttggg atatacccca aagtcctcta cccctcaact tttatggccc 1600
tttccctaga tatactgcgg gatctctcct taggataaaag agttgctgtt 1650
gaagttgtat atttttgatc aatatatttg gaaattnaaag tttctgactt 1700

t 1701

<210> 423

<211> 337

<212> PRT

<213> Homo sapiens

<400> 423

Met Leu Phe Ser Ala Leu Leu Leu Glu Val Ile Trp Ile Leu Ala
1 5 10 15

Ala Asp Gly Gly Gln His Trp Thr Tyr Glu Gly Pro His Gly Gln
20 25 30

Asp His Trp Pro Ala Ser Tyr Pro Glu Cys Gly Asn Asn Ala Gln
35 40 45

Ser Pro Ile Asp Ile Gln Thr Asp Ser Val Thr Phe Asp Pro Asp
50 55 60

Leu Pro Ala Leu Gln Pro His Gly Tyr Asp Gln Pro Gly Thr Glu
65 70 75

Pro Leu Asp Leu His Asn Asn Gly His Thr Val Gln Leu Ser Leu

80	85	90
Pro Ser Thr Leu Tyr	Leu Gly Gly Leu	Pro Arg Lys Tyr Val Ala
95	100	105
Ala Gln Leu His Leu His Trp	Gly Gln Lys Gly Ser Pro Gly Gly	
110	115	120
Ser Glu His Gln Ile Asn Ser Glu Ala	Thr Phe Ala Glu Leu His	
125	130	135
Ile Val His Tyr Asp Ser Asp Ser Tyr	Asp Ser Leu Ser Glu Ala	
140	145	150
Ala Glu Arg Pro Gln Gly Leu Ala Val	Leu Gly Ile Leu Ile Glu	
155	160	165
Val Gly Glu Thr Lys Asn Ile Ala Tyr	Glu His Ile Leu Ser His	
170	175	180
Leu His Glu Val Arg His Lys Asp Gln	Lys Thr Ser Val Pro Pro	
185	190	195
Phe Asn Leu Arg Glu Leu Leu Pro Lys	Gln Leu Gly Gln Tyr Phe	
200	205	210
Arg Tyr Asn Gly Ser Leu Thr Thr Pro	Pro Cys Tyr Gln Ser Val	
215	220	225
Leu Trp Thr Val Phe Tyr Arg Arg Ser	Gln Ile Ser Met Glu Gln	
230	235	240
Leu Glu Lys Leu Gln Gly Thr Leu Phe	Ser Thr Glu Glu Glu Pro	
245	250	255
Ser Lys Leu Leu Val Gln Asn Tyr Arg	Ala Leu Gln Pro Leu Asn	
260	265	270
Gln Arg Met Val Phe Ala Ser Phe Ile	Gln Ala Gly Ser Ser Tyr	
275	280	285
Thr Thr Gly Glu Met Leu Ser Leu Gly	Val Gly Ile Leu Val Gly	
290	295	300
Cys Leu Cys Leu Leu Ala Val Tyr	Phe Ile Ala Arg Lys Ile	
305	310	315
Arg Lys Lys Arg Leu Glu Asn Arg Lys	Ser Val Val Phe Thr Ser	
320	325	330
Ala Gln Ala Thr Thr Glu Ala		
335		

<210> 424

<211> 18

<212> DNA

<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 424
gtaaagtgc tggccagc 18

<210> 425
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 425
cccgatctgc ctgctgtc 18

<210> 426
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 426
ctgcactgtc tggccattat tgtc 24

<210> 427
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 427
cagaaaccca tgatacccta ctgaacacccg aatccccctgg aagcc 45

<210> 428
<211> 1073
<212> DNA
<213> Homo sapiens

<400> 428
aattttcac cagagtaaac ttgagaaacc aactggacct tgagtattgt 50
acatttgcc tcgtggaccc aaaggttagca atctgaaaca tgaggagtac 100
gattctactg ttttgtcttc taggatcaac tcggtcatta ccacagctca 150

aacctgctt gggactccct cccacaaaac tggctccgga tcagggaca 200
ctaccaaacc aacagcagtc aaatcaggc tttccttctt taagtctgat 250
accattaaaca cagatgctca cactgggcc agatctgcat ctgttaaatc 300
ctgctgcagg aatgacaccc ggtacccaga cccacccatt gaccctggga 350
gggttgaatg tacaacagca actgcaccca catgtgttac caattttgt 400
cacacaactt ggagcccagg gcactatcct aagctcagag gaattgccac 450
aaatcttcac gagcctcatc atccattcct tgccccggg aggcatcctg 500
cccaccagtc aggcaaaaaa taatccagat gtccaggatg gaagccttcc 550
agcaggagga gcaggtgtaa atcctgcccccc acagatgacg actttgcagt gaccacccct 600
gcctcccaac tcccaacttgc acagatgacg actttgcagt gaccacccct 650
gcaggcatcc aaaggagcac acatgccatc gagaaagcca ccacagaatc 700
agcaaatttgc attcataatc ctgtttcaaa tttttcaac taagctgcct 750
cgaatttggt gatacatgtg aatctttatc attgattata ttatggataa 800
gattgagaca cattggatag tcttagaaga aattaattct taatttaccc 850
gaaaatatttgc ttgaaatttc agaaaatatg ttctatgttag agaatccaa 900
cttttaaaaaa caataattca atggataat ctgtttcaac taatataacat 950
tatgctgcct ggatgatatg catattaaaa catatttggaa aaactggaaa 1000
aaaaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1050
aaaaaaaaaaaa aaaaaaaaaa aaa 1073

<210> 429

<211> 209

<212> PRT

<213> Homo sapiens

<400> 429

Met Arg Ser Thr Ile Leu Leu Phe Cys Leu Leu Gly Ser Thr Arg

1 5 10 15

Ser Leu Pro Gln Leu Lys Pro Ala Leu Gly Leu Pro Pro Thr Lys

20 25 30

Leu Ala Pro Asp Gln Gly Thr Leu Pro Asn Gln Gln Ser Asn

35 40 45

Gln Val Phe Pro Ser Leu Ser Leu Ile Pro Leu Thr Gln Met Leu

50 55 60

Thr Leu Gly Pro Asp Leu His Leu Leu Asn Pro Ala Ala Gly Met

65 70 75

Thr	Pro	Gly	Thr	Gln	Thr	His	Pro	Leu	Thr	Leu	Gly	Gly	Leu	Asn
80									85					90

Val	Gln	Gln	Gln	Leu	His	Pro	His	Val	Leu	Pro	Ile	Phe	Val	Thr
95									100					105

Gln	Leu	Gly	Ala	Gln	Gly	Thr	Ile	Leu	Ser	Ser	Glu	Glu	Leu	Pro
110									115					120

Gln	Ile	Phe	Thr	Ser	Leu	Ile	Ile	His	Ser	Leu	Phe	Pro	Gly	Gly
125									130					135

Ile	Leu	Pro	Thr	Ser	Gln	Ala	Gly	Ala	Asn	Pro	Asp	Val	Gln	Asp
140									145					150

Gly	Ser	Leu	Pro	Ala	Gly	Gly	Ala	Gly	Val	Asn	Pro	Ala	Thr	Gln
155									160					165

Gly	Thr	Pro	Ala	Gly	Arg	Leu	Pro	Thr	Pro	Ser	Gly	Thr	Asp	Asp
170									175					180

Asp	Phe	Ala	Val	Thr	Thr	Pro	Ala	Gly	Ile	Gln	Arg	Ser	Thr	His
185									190					195

Ala	Ile	Glu	Glu	Ala	Thr	Thr	Glu	Ser	Ala	Asn	Gly	Ile	Gln
200									205				

<210> 430

<211> 1257

<212> DNA

<213> Homo Sapien

<400> 430

ggagagaggc gcgcgggtga aaggcgatt gatgcagcct gcggcggcct 50

cggagcgcgg cggagccaga cgctgaccac gttcctctcc tcggtctcct 100

ccgcctccag ctccgcgctg cccggcagcc gggagccatg cgaccccagg 150

gccccgccgc ctccccgcag cggctccgcg gcctcctgct gtcctgctg 200

ctgcagctgc ccgcgcgtc gagcgcctct gagatccca agggaaagca 250

aaaggcgcag ctccggcaga gggaggttgtt ggacctgtat aatgaaatgt 300

gcttacaagg gccagcagga gtgcctggtc gagacggag ccctggggcc 350

aatgttattc cgggtacacc tggatccca ggtcggatg gattcaaagg 400

agaaaagggg gaatgtctga gggaaagct tgaggagtcc tggacaccca 450

actacaagca gtgttcatgg agttcatttg attatggcat agatcttggg 500

aaaattgcgg agtgtacatt tacaaagatg cgttcaaata gtgctctaag 550

agttttgttc agtggctcac ttccggctaaa atgcagaaat gcatgctgtc 600

agcgttggta ttccacattc aatggagctg aatgttcagg acctcttccc 650

attgaagcta taatttattt ggaccaagga agccctgaaa tgaattcaac 700
aattaatatt catcgactt cttctgtgga aggacttgtt gtgctggatt 750
gtgctggatt agtggatgtt gctatctggg ttggcacttg ttcagattac 800
ccaaaaggag atgcttctac tggatgaaat tcagttctc gcatcattat 850
tgaagaacta ccaaataaaa tgcttaatt ttcatttgct acctctttt 900
ttattatgcc ttggaatggt tcacttaat gacattttaa ataagtttat 950
gtatacatct gaatgaaaag caaagctaaa tatgtttaca gaccggatg 1000
tgatttcaca ctgttttaa atcttagcatt attcatttg cttcaatcaa 1050
aagtggtttc aatattttt ttagttggtt agaatacttt cttcatagtc 1100
acattctctc aacctataat ttggaatatt gttgtggct tttgttttt 1150
ctcttagtat agcatttta aaaaaatata aaagctacca atctttgtac 1200
aatttgtaaa tgttaagaat tttttata tctgttaaat aaaaattatt 1250
tccaaca 1257

<210> 431

<211> 243

<212> PRT

<213> Homo Sapien

<400> 431

Met	Arg	Pro	Gln	Gly	Pro	Ala	Ala	Ser	Pro	Gln	Arg	Leu	Arg	Gly
1					5				10				15	
Leu	Gln	Leu	Pro	Ala	Pro	Ser	Ser	Ala						
								20			25			30
Ser	Glu	Ile	Pro	Lys	Gly	Lys	Gln	Lys	Ala	Gln	Leu	Arg	Gln	Arg
				35				40				45		
Glu	Val	Val	Asp	Leu	Tyr	Asn	Gly	Met	Cys	Leu	Gln	Gly	Pro	Ala
				50					55				60	
Gly	Val	Pro	Gly	Arg	Asp	Gly	Ser	Pro	Gly	Ala	Asn	Val	Ile	Pro
				65				70				75		
Gly	Thr	Pro	Gly	Ile	Pro	Gly	Arg	Asp	Gly	Phe	Lys	Gly	Glu	Lys
				80				85				90		
Gly	Glu	Cys	Leu	Arg	Glu	Ser	Phe	Glu	Glu	Ser	Trp	Thr	Pro	Asn
				95					100			105		
Tyr	Lys	Gln	Cys	Ser	Trp	Ser	Ser	Leu	Asn	Tyr	Gly	Ile	Asp	Leu
				110					115			120		
Gly	Lys	Ile	Ala	Glu	Cys	Thr	Phe	Thr	Lys	Met	Arg	Ser	Asn	Ser
				125				130				135		

Ala Leu Arg Val Leu Phe Ser Gly Ser Leu Arg Leu Lys Cys Arg
140 145 150
Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr Phe Asn Gly Ala Glu
155 160 165
Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile Tyr Leu Asp Gln
170 175 180
Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His Arg Thr Ser
185 190 195
Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu Val Asp
200 205 210
Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly Asp
215 220 225
Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu
230 235 240
Leu Pro Lys

<210> 432
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial Sequence

<400> 432
aggacttgcc ctcaggaa 18

<210> 433
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 433
cgcaggacag ttgtgaaaat a 21

<210> 434
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 434
atgacgctcg tccaaaggcca c 21

<210> 435

<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 435
cccacctgt a ccaccatgt 19

<210> 436
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 436
actccaggca ccatctgttc tccc 24

<210> 437
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 437
aagggctggc attcaagtc 19

<210> 438
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 438
tgacctggca aaggaagaa 19

<210> 439
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 439
cagccaccct ccagtccaag g 21

<210> 440
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 440
gggtcgtgtt ttggagaga 19

<210> 441
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 441
ctggccctca gagcaccaat 20

<210> 442
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 442
tcctccatca cttcccctag ctcca 25

<210> 443
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 443
ctggcaggag ttaaagtcc aaga 24

<210> 444
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 444
aaaggacacc gggatgtg 18

<210> 445
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 445
agcgtacact ctctccaggc aaccag 26

<210> 446
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 446
caattctgga tgaggtggta ga 22

<210> 447
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 447
caggactgag cgcttgttt 20

<210> 448
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 448
caaagcgcca agtaccggac c 21

<210> 449
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 449
ccagacctca gccaggaa 18

<210> 450
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 450
ccctagctga ccccttca 18

<210> 451
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 451
tctgacaaggc agttttctga atc 23

<210> 452
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 452
ctctccccct ccctttcct ttgttt 26

<210> 453
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 453
ctctggtgcc cacagtga 18

<210> 454
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 454
ccatgcctgc tcagccaaga a 21

<210> 455
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 455
caggaaatct ggaaacctac agt 23

<210> 456
<211> 20
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 456
ccttggaaaag gacccaggttt 20

<210> 457

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 457
atgagtcgca cctgctgttc cc 22

<210> 458

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 458
tagcagctgc ccttggtt 18

<210> 459

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 459
aacagcaggt gcgactcatc ta 22

<210> 460

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 460
tgcttaggcga cgacacccag acc 23

<210> 461

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe
<400> 461
tggacacgtg gcagtgga 18

<210> 462
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe
<400> 462
tcatggtctc gtcccattc 19

<210> 463
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe
<400> 463
caccatttgt ttctctgtct ccccatc 27

<210> 464
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe
<400> 464
ccggcatcct tggagtag 18

<210> 465
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe
<400> 465
tccccattag cacaggagta 20

<210> 466
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe
<400> 466

aggctttgc ctgtcctgct gct 23
<210> 467
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 467
gccccagagtc ccacttgt 18

<210> 468
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 468
actgctccgc ctactacga 19

<210> 469
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 469
aggcatccctc gccgtcctca 20

<210> 470
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 470
aaggccaagg tgagtccat 19

<210> 471
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 471
cgagtgtgtg cgaaacctaa 20

<210> 472

<211> 24
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